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MN GENE AND PROTEIN

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This application is a continuation-in-part of now pending U.S. Serial No. 08/260,190 (filed June 15, 1994), which, in turn, is a continuation-in-part of now pending U.S. Serial No. 08/177,093 (filed December 30, 1993), which is in turn a continuation-in-part of U.S. Serial No. 07/964,589 (filed October 21, 1992), which issued as U.S. Patent No. 5,387,676 on February 7, 1995, but from which a now pending continuation U.S. Serial No. 08/335,469 was filed on November 7, 1994. This application declares priority under 35 USC § 120 from those U.S. applications, and also under 35 USC § 119 from the now pending Czechoslovakian patent application PV-709-92 (filed March 11, 1992).

FIELD OF THE INVENTION

The present invention is in the general area of medical genetics and in the fields of biochemical engineering and immunochemistry. More specifically, it relates to the identification of a new gene--the MN gene--a cellular gene coding for the MN protein. The inventors hereof found MN proteins to be associated with tumorigenicity. Evidence indicates that the MN protein

appears to represent a potentially novel type of oncoprotein. Identification of MN antigen as well as antibodies specific therefor in patient samples provides the basis for diagnostic/prognostic assays for cancer.

BACKGROUND OF THE INVENTION

A novel quasi-viral agent having rather unusual properties was detected by its capacity to complement mutants of vesicular stomatitis virus (VSV) with heat-labile surface G protein in HeLa cells (cell line derived from human cervical adenocarcinoma), which had been cocultivated with human breast carcinoma cells. [Zavada et al., Nature New Biol., 240: 124 (1972); Zavada et al., J. Gen. Virol., 24: 327 (1974); Zavada, J., Arch. Virol., 50: 1 (1976); Zavada, J., J. Gen. Virol., 63: 15-24 (1982); Zavada and Zavadova, Arch. Virol., 118: 189 (1991).] The quasi viral agent was called MaTu as it was presumably derived from a human mammary tumor.

There was significant medical interest in studying and characterizing MaTu as it appeared to be an entirely new type of molecular parasite of living cells, and possibly originated from a human tumor. Described herein is the elucidation of the biological and molecular nature of MaTu which resulted in the discovery of the MN gene and protein. MaTu was found by the inventors to be a two-component system, having an exogenous transmissible component, MX, and

an endogenous cellular component, MN. As described herein, the MN component was found to be a cellular gene, showing only very little homology with known DNA sequences. The MN gene was found to be present in the chromosomal DNA of all vertebrates tested, and its expression was found to be strongly correlated with tumorigenicity.

The exogenous MaTu-MX transmissible agent was identified as lymphocytic choriomeningitis virus (LCMV) which persistently infects HeLa cells. The inventors discovered that the MN expression in HeLa cells is positively regulated by cell density, and also its expression level is increased by persistent infection with LCMV.

Research results provided herein show that cells transfected with MN cDNA undergo changes indicative of malignant transformation. Further research findings described herein indicate that the disruption of cell cycle control is one of the mechanisms by which MN may contribute to the complex process of tumor development.

Described herein is the cloning and sequencing of the MN gene and the recombinant production of MN proteins. Also described are antibodies prepared against MN proteins/polypeptides. MN proteins/polypeptides can be used in serological assays according to this invention to detect MN-specific antibodies. Further, MN proteins/polypeptides and/or antibodies reactive with MN antigen can be used in

immunoassays according to this invention to detect and/or quantitate MN antigen. Such assays may be diagnostic and/or prognostic for neoplastic/pre-neoplastic disease.

SUMMARY OF THE INVENTION

Herein disclosed is the MN gene, a cellular gene which is the endogenous component of the MaTu agent. A full-length cDNA sequence for the MN gene is shown in Figure 1 [SEQ. ID. NO.: 1]. Figure 15a-d provides a complete genomic sequence for MN [SEQ. ID. NO.: 5]. Figure 25 provides the sequence for a proposed MN promoter region [SEQ. ID. NO.: 27].

This invention is directed to the MN gene, fragments thereof and the related cDNA which are useful, for example, as follows: 1) to produce MN proteins/ polypeptides by biochemical engineering; 2) to prepare nucleic acid probes to test for the presence of the MN gene in cells of a subject; 3) to prepare appropriate polymerase chain reaction (PCR) primers for use, for example, in PCR-based assays or to produce nucleic acid probes; 4) to identify MN proteins and polypeptides as well as homologs or near homologs thereto; 5) to identify various mRNAs transcribed from MN genes in various tissues and cell lines, preferably human; and 6) to identify mutations in MN genes. The invention further concerns purified and isolated DNA

molecules comprising the MN gene or fragments thereof, or the related cDNA or fragments thereof.

Thus, this invention in one aspect concerns isolated nucleic acid sequences that encode MN proteins or polypeptides wherein the nucleotide sequences for said nucleic acids are selected from the group consisting of:

(a) SEQ. ID. NO.: 1;

(b) nucleotide sequences that hybridize under stringent conditions to SEQ. ID. NO.: 1 or to its complement;

(c) nucleotide sequences that differ from SEQ. ID. NO.: 1 or from the nucleotide sequences of (b) in codon sequence because of the degeneracy of the genetic code. Further, such nucleic acid sequences are selected from nucleotide sequences that but for the degeneracy of the genetic code would hybridize to SEQ. ID. NO.: 1 or to its complement under stringent hybridization conditions.

Further, such isolated nucleic acids that encode MN proteins or polypeptides can also include the MN nucleic acids of the genomic clone shown in Figure 15a-d, that is, SEQ. ID. NO.: 5, as well as sequences that hybridize to it or its complement under stringent conditions, or would hybridize to SEQ. ID. NO.: 5 or to its complement under such conditions, but for the degeneracy of the genetic code. Degenerate variants of SEQ. ID. NOS.: 1 and 5 are within the scope of the invention.

Further, this invention concerns nucleic acid probes which are fragments of the isolated nucleic acids that encode MN proteins or polypeptides as described above. Preferably said nucleic acid probes are comprised of at least 29 nucleotides, more preferably of at least 50 nucleotides, still more preferably at least 100 nucleotides, and even more preferably at least 150 nucleotides.

Still further, this invention is directed to isolated nucleic acids selected from the group consisting of:

(a) a nucleic acid having the nucleotide sequence shown in Figure 15a-d [SEQ. ID. NO.: 5] and its complement;

(b) nucleic acids that hybridize under standard stringent hybridization conditions to the nucleic acids of (a); and

(c) nucleic acids that differ from the nucleic acids of (a) and (b) in codon sequence because of the degeneracy of the genetic code. The invention also concerns nucleic acids that but for the degeneracy of the genetic code would hybridize to the nucleic acids of (a) under standard stringent hybridization conditions. The nucleic acids of (b) and (c) that hybridize to the coding region of SEQ. ID. NO.: 5 preferably have a length of at least 29 nucleotides, whereas the nucleic acids of (b) and (c) that hybridize partially or wholly to the non-coding regions of SEQ. ID. NO.: 5 or its complement are those that function

as nucleic acid probes to identify MN nucleic acid sequences. Conventional technology can be used to determine whether the nucleic acids of (b) and (c) or of fragments of SEQ. ID. NO.: 5 are useful to identify MN nucleic acid sequences, for example, as outlined in Benton and Davis, Science, 196: 180 (1977) and Fuscoe et al. Genomics, 5: 100 (1989). In general, the nucleic acids of (b) and (c) are preferably at least 29 nucleotides, more preferably at least 50 nucleotides, still more preferably at least 100 nucleotides, and even more preferably at least 150 nucleotides. An exemplary and preferred nucleic acid probe is SEQ. ID. NO.: 55 (a 470 bp probe useful in RNase portection assays).

Test kits of this invention can comprise the nucleic acid probes of the invention which are useful diagnostically/prognostically for neoplastic and/or pre-neoplastic disease. Preferred test kits comprise means for detecting or measuring the hybridization of said probes to the MN gene or to the mRNA product of the MN gene, such as a visualizing means.

Fragments of the isolated nucleic acids of the invention, can also be used as PCR primers to amplify segments of MN genes, and may be useful in identifying mutations in MN genes. Typically, said PCR primers are oligonucleotides, preferably at least 16 nucleotides, but they may be considerably longer. Exemplary primers may be

from about 16 nucleotides to about 50 nucleotides, preferably from about 19 nucleotides to about 45 nucleotides.

This invention also concerns nucleic acids which encode MN proteins or polypeptides that are specifically bound by monoclonal antibodies designated M75 that are produced by the hybridoma VU-M75 deposited at the American Type Culture Collection (ATCC) at 12301 Parklawn Drive in Rockville, Maryland 20852 (USA) under ATCC No. HB 11128, and/or by monoclonal antibodies designated MN12 produced by the hybridoma MN 12.2.2 deposited at the ATCC under ATCC No. HB 11647.

The invention further concerns the discovery of a hitherto unknown protein--MN, encoded by the MN gene. The expresssion of MN proteins is inducible by growing cells in dense cultures, and such expression was discovered to be associated with tumorigenic cells.

MN proteins were found to be produced by some human tumor cell lines <u>in vitro</u>, for example, by HeLa (cervical carcinoma), T24 (bladder carcinoma) and T47D (mammary carcinoma) and SK-Mel 1477 (melanoma) cell lines, by tumorigenic hybrid cells and by cells of some human cancers <u>in vivo</u>, for example, by cells of uterine cervical, ovarian and endometrial carcinomas as well as cells of some benign neoplasias such as mammary papillomas. MN proteins were not found in non-tumorigenic hybrid cells, and are

generally not found in the cells of normal tissues, although they have been found in a few normal tissues, most notably and abundantly in normal stomach tissues. MN antigen was found by immunohistochemical staining to be prevalent in tumor cells and to be present sometimes in morphologically normal appearing areas of tissue specimens exhibiting dysplasia and/or malignancy. Thus, the MN gene is strongly correlated with tumorigenesis and is considered to be a putative oncogene.

In HeLa and in tumorigenic HeLa x fibroblast hybrid (H/F-T) cells, MN protein is manifested as a "twin" protein p54/58N; it is glycosylated and forms disulfide-linked oligomers. As determined by electrophoresis upon reducing gels, MN proteins have molecular weights in the range of from about 40 kd to about 70 kd, preferably from about 45 kd to about 65 kd, more preferably from about 48 kd to about 58 kd. Upon non-reducing gels, MN proteins in the form of oligomers have molecular weights in the range of from about 145 kd to about 160 kd, preferably from about 150 to about 155 kd, still more preferably from about 152 to about 154 kd. A predicted amino acid sequence for a preferred MN protein of this invention is shown in Figure 1 [SEQ. ID. NO. 2].

The discovery of the MN gene and protein and thus, of substantially complementary MN genes and proteins encoded thereby, led to the finding that the expression of MN

proteins was associated with tumorigenicity. That finding resulted in the creation of methods that are diagnostic/prognostic for cancer and precancerous conditions. Methods and compositions are provided for identifying the onset and presence of neoplastic disease by detecting and/or quantitating MN antigen in patient samples, including tissue sections and smears, cell and tissue extracts from vertebrates, preferably mammals and more preferably humans. Such MN antigen may also be found in body fluids.

MN proteins and genes are of use in research concerning the molecular mechanisms of oncogenesis, in cancer diagnostics/prognostics, and may be of use in cancer immunotherapy. The present invention is useful for detecting a wide variety of neoplastic and/or pre-neoplastic diseases. Exemplary neoplastic diseases include carcinomas, such as mammary, bladder, ovarian, uterine, cervical, endometrial, squamous cell and adenosquamous carcinomas; and head and neck cancers; mesodermal tumors, such as neuroblastomas and retinoblastomas; sarcomas, such as osteosarcomas and Ewing's sarcoma; and melanomas. Of particular interest are head and neck cancers, gynecologic cancers including ovarian, cervical, vaginal, endometrial and vulval cancers; gastrointestinal cancer, such as, stomach, colon and esophageal cancers; urinary tract cancer, such as, bladder and kidney cancers; skin cancer; liver cancer; prostate cancer; lung cancer; and breast cancer. Of

still further particular interest are gynecologic cancers; breast cancer; urinary tract cancers, especially bladder cancer; lung cancer; and liver cancer. Even further of particular interest are gynecologic cancers and breast cancer. Gynecologic cancers of particular interest are carcinomas of the uterine cervix, endometrium and ovaries; more particularly such gynecologic cancers include cervical squamous cell carcinomas, adenosquamous carcinomas, adenocarcinomas as well as gynecologic precancerous conditions, such as metaplastic cervical tissues and condylomas.

The invention further relates to the biochemical engineering of the MN gene, fragments thereof or related cDNA. For example, said gene or a fragment thereof or related cDNA can be inserted into a suitable expression vector; host cells can be transformed with such an expression vector; and an MN protein/polypeptide, preferably an MN protein, is expressed therein. Such a recombinant protein or polypeptide can be glycosylated or nonglycosylated, preferably glycosylated, and can be purified to substantial purity. The invention further concerns MN proteins/polypeptides which are synthetically or otherwise biologically prepared.

Said MN proteins/polypeptides can be used in assays to detect MN antigen in patient samples and in serological assays to test for MN-specific antibodies. MN

proteins/polypeptides of this invention are serologically active, immunogenic and/or antigenic. They can further be used as immunogens to produce MN-specific antibodies, polyclonal and/or monoclonal, as well as an immune T-cell response.

The invention further is directed to MN-specific antibodies, which can be used diagnostically/prognostically and may be used therapeutically. Preferred according to this invention are MN-specific antibodies reactive with the epitopes represented respectively by the amino acid sequences of the MN protein shown in Figure 1 as follows: from AA 62 to AA 67 [SEQ. ID. NO.: 10]; from AA 55 to AA 60 [SEQ. ID. NO.: 11]; from AA 127 to AA 147 [SEQ. ID. NO.: 12]; from AA 36 to AA 51 [SEQ. ID. NO.: 13]; from AA 68 to AA 91 [SEQ. ID. NO.: 14]; from AA 279 to AA 291 [SEQ. ID. NO.: 15]; and from AA 435 to AA 450 [SEQ. ID. NO.: 16]. More preferred are antibodies reactive with epitopes represented by SEQ. ID. NOS.: 10, 11 and 12. Still more preferred are antibodies reactive with the epitopes represented by SEQ. ID NOS: 10 and 11, as for example, respectively Mabs M75 and MN12. Most preferred are monoclonal antibodies reactive with the epitope represented by SEQ. ID. NO.: 10.

Also preferred according to this invention are antibodies prepared against recombinantly produced MN proteins as, for example, GEX-3X-MN, MN 20-19, MN-Fc and MN-

PA. Also preferred are MN-specific antibodies prepared against glycosylated MN proteins, such as, MN 20-19 expressed in baculovirus infected Sf9 cells.

A hybridoma that produces a representative MN-specific antibody, the monoclonal antibody M75 (Mab M75), was deposited at the under ATCC Number HB 11128 as indicated above. The M75 antibody was used to discover and identify the MN protein and can be used to identify readily MN antigen in Western blots, in radioimmunoassays and immunohistochemically, for example, in tissue samples that are fresh, frozen, or formalin-, alcohol-, acetone- or otherwise fixed and/or paraffin-embedded and deparaffinized. Another representative MN-specific antibody, Mab MN12, is secreted by the hybridoma MN 12.2.2, which was deposited at the ATCC under the designation HB 11647.

MN-specific antibodies can be used, for example, in laboratory diagnostics, using immunofluorescence microscopy or immunohistochemical staining; as a component in immunoassays for detecting and/or quantitating MN antigen in, for example, clinical samples; as probes for immunoblotting to detect MN antigen; in immunoelectron microscopy with colloid gold beads for localization of MN proteins and/or polypeptides in cells; and in genetic engineering for cloning the MN gene or fragments thereof, or related cDNA. Such MN-specific antibodies can be used as components of diagnostic/ prognostic kits, for example, for

in vitro use on histological sections; such antibodies can also and used for in vivo diagnostics/prognostics, for example, such antibodies can be labeled appropriately, as with a suitable radioactive isotope, and used in vivo to locate metastases by scintigraphy. Further such antibodies may be used in vivo therapeutically to treat cancer patients with or without toxic and/or cytostatic agents attached thereto. Further, such antibodies can be used in vivo to detect the presence of neoplastic and/or pre-neoplastic disease. Still further, such antibodies can be used to affinity purify MN proteins and polypeptides.

This invention also concerns recombinant DNA molecules comprising a DNA sequence that encodes for an MN protein or polypeptide, and also recombinant DNA molecules that encode not only for an MN protein or polypeptide but also for an amino acid sequence of a non-MN protein or polypeptide. Said non-MN protein or polypeptide may preferably be nonimmunogenic to humans and not typically reactive to antibodies in human body fluids. Examples of such a DNA sequence is the alpha-peptide coding region of beta-galactosidase and a sequence coding for glutathione S-transferase or a fragment thereof. However, in some instances, a non-MN protein or polypeptide that is serologically active, immunogenic and/or antigenic may be preferred as a fusion partner to a MN antigen. Further, claimed herein are such recombinant fusion proteins/

polypeptides which are substantially pure and non-naturally occurring. Exemplary fusion proteins of this invention are GEX-3X-MN, MN-Fc and MN-PA, described infra.

This invention also concerns methods of treating neoplastic disease and/or pre-neoplastic disease comprising inhibiting the expression of MN genes by administering antisense nucleic acid sequences that are substantially complementary to mRNA transcribed from MN genes. Said antisense nucleic acid sequences are those that hybridize to such mRNA under stringent hybridization conditions. Preferred are antisense nucleic acid sequences that are substantially complementary to sequences at the 5′ end of the MN cDNA sequence shown in Figure 1. Preferably said antisense nucleic acid sequences are oligonucleotides.

This invention also concerns vaccines comprising an immunogenic amount of one or more substantially pure MN proteins and/or polypeptides dispersed in a physiologically acceptable, nontoxic vehicle, which amount is effective to immunize a vertebrate, preferably a mammal, more preferably a human, against a neoplastic disease associated with the expression of MN proteins. Said proteins can be recombinantly, synthetically or otherwise biologically produced. Recombinent MN proteins include GEX-3X-MN and MN 20-19. A particular use of said vaccine would be to prevent recidivism and/or metastasis. For example, it could be

administered to a patient who has had an MN-carrying tumor surgically removed, to prevent recurrence of the tumor.

The immunoassays of this invention can be embodied in test kits which comprise MN proteins/polypeptides and/or MN-specific antibodies. Such test kits can be in solid phase formats, but are not limited thereto, and can also be in liquid phase format, and can be based on immunohistochemical assays, ELISAS, particle assays, radiometric or fluorometric assays either unamplified or amplified, using, for example, avidin/biotin technology.

Abbreviations

The following abbreviations are used herein:

AA	-	amino acid
ATCC	-	American Type Culture Collection
bp	-	base pairs
BLV	-	bovine leukemia virus
BSA	-	bovine serum albumin
BRL	-	Bethesda Research Laboratories
CA	-	carbonic anhydrase
CAT	-	chloramphenicol acetyltransferase
Ci	-	curie
cm	-	centimeter
CMV	-	cytomegalovirus
cpm	-	counts per minute
C-terminus	-	carboxyl-terminus

°C	-	degrees centigrade
DAB	-	diaminobenzidine
dH_2O	-	deionized water
DEAE	-	diethylaminoethyl
DMEM	-	Dulbecco modified Eagle medium
DTT	-	dithiothreitol
EDTA	-	ethylenediaminetetracetate
EIA	-	enzyme immunoassay
ELISA	-	enzyme-linked immunosorbent assay
EtOH	-	ethanol
F	-	fibroblasts
FCS	-	fetal calf serum
FIBR	-	fibroblasts
FITC	-	fluorescein isothiocyanate
GEX-3X-MN	-	fusion protein MN glutathione S-transferase
H	-	HeLa cells
H_2O_2	-	hydrogen peroxide
HCA	-	Hydrophobic Cluster Analysis
HEF	-	human embryo fibroblasts
HeLa K	-	standard type of HeLa cells
HeLa S	-	Stanbridge's mutant HeLa D98/AH.2
H/F-T	-	hybrid HeLa fibroblast cells that are tumorigenic; derived from HeLa D98/AH.2
H/F-N	-	hybrid HeLa fibroblast cells that are nontumorigenic; derived from HeLa D98/AH.2
HGPRT$^-$	-	hypoxanthine guanine phosphoribosyl transferase-deficient

HLH	-	helix-loop-helix
HRP	-	horseradish peroxidase
Inr	-	initiator
IPTG	-	isopropyl-Beta-D-thiogalacto-pyranoside
kb	-	kilobase
kbp	-	kilobase pairs
kd	-	kilodaltons
KPL	-	Kirkegaard & Perry Laboratories, Inc.
LCMV	-	lymphocytic choriomeningitis virus
LTR	-	long terminal repeat
M	-	molar
mA	-	milliampere
MAb	-	monoclonal antibody
ME	-	mercaptoethanol
MEM	-	minimal essential medium
min.	-	minute(s)
mg	-	milligram
ml	-	milliliter
mM	-	millimolar
MMC	-	mitomycin C
MLV	-	murine leukemia virus
MTV	-	mammary tumor virus
N	-	normal concentration
ng	-	nanogram
NGS	-	normal goat serum
nt	-	nucleotide

N-terminus	-	amino-terminus
ODN	-	oligodeoxynucleotide
ORF	-	open reading frame
PA	-	Protein A
PAGE	-	polyacrylamide gel electrophoresis
PBS	-	phosphate buffered saline
PCR	-	polymerase chain reaction
PEST	-	combination of one-letter abbreviations for proline, glutamic acid, serine, threonine
pI	-	isoelectric point
PMA	-	phorbol 12-myristate 13-acetate
Py	-	pyrimidine
RIP	-	radioimmunoprecipitation
RIPA	-	radioimmunoprecipitation assay
RNP	-	RNase protection assay
SAC	-	protein A-<u>Staphylococcus aureus</u> cells
SDRE	-	serum dose response element
SDS	-	sodium dodecyl sulfate
SDS-PAGE	-	sodium dodecyl sulfate-polyacrylamide gel electrophoresis
SINE	-	short interspersed repeated sequence
SSDS	-	synthetic splice donor site
SP-RIA	-	solid-phase radioimmunoassay
SSDS	-	synthetic splice donor site
SSPE	-	NaCl (0.18 M), sodium phosphate (0.01 M), EDTA (0.001 M)
TBE	-	Tris-borate/EDTA electrophoresis buffer
TCA	-	trichloroacetic acid

TC media	-	tissue culture media
TMB	-	tetramethylbenzidine
Tris	-	tris (hydroxymethyl) aminomethane
μCi	-	microcurie
μg	-	microgram
μl	-	microliter
μM	-	micromolar
VSV	-	vesicular stomatitis virus
X-MLV	-	xenotropic murine leukemia virus

Cell Lines

The following cell lines were used in the experiments herein described:

HeLa K -- standard type of HeLa cells; aneuploid, epithelial-like cell line isolated from a human cervical adenocarcinoma [Gey et al., Cancer Res., 12: 264 (1952); Jones et al., Obstet. Gynecol., 38: 945-949 (1971)] obtained from Professor B. Korych, [Institute of Medical Microbiology and Immunology, Charles University; Prague, Czech Republic]

HeLa D98/AH.2 (also HeLa S) -- Mutant HeLa clone that is hypoxanthine guanine phosphoribosyl transferase-deficient (HGPRT$^-$) kindly provided by Eric J. Stanbridge [Department of Microbiology, College of Medicine, University of California, Irvine, CA (USA)] and reported in Stanbridge et al., Science, 215: 252-259 (15 Jan. 1982); parent of hybrid cells H/F-N and H/F-T, also obtained from E.J. Stanbridge.

NIH-3T3 -- murine fibroblast cell line reported in Aaronson, Science, 237: 178 (1987).

T47D -- cell line derived from a human mammary carcinoma [Keydar et al., Eur. J. Cancer, 15: 659-670 (1979)]; kindly provided by J. Keydar [Haddasah Medical School; Jerusalem, Israel]

T24 -- cell line from urinary bladder carcinoma [Bubenik et al., Int. J. Cancer, 11: 765-773 (1973)] kindly provided by J. Bubenik [Institute of Molecular Genetics, Czechoslovak Academy of Sciences; Prague, Czech Republic]

HMB2 -- cell line from melanoma [Svec et al., Neoplasma, 35: 665-681 (1988)]

HEF -- human embryo fibroblasts [Zavada et al., Nature New Biology, 240: 124-125 (1972)]

SIRC -- cell line from rabbit cornea (control and X-MLV-infected) [Zavada et al., Virology, 82: 221-231 (1977)]

Vero cells -- African green monkey cell line [Zavada et al. (1977)]

myeloma cell line NS-0 -- myeloma cell line used as a fusion parent in production of monoclonal antibodies [Galfre and Milstein, Methods Enzymol., 73: 3-46 (1981)]

SK-Mel 1477 -- human melanoma cell line kindly provided by K.E. Hellstrom [Division of Tumor Immunology, Fred Hutchins Cancer Research Center; Seattle, Washington (USA)]

XC -- cells derived from a rat rhabdomyosarcoma induced with Rous sarcoma virus-induced rat sarcoma [Svoboda, J., Natl. Cancer Center Institute Monograph No. 17, IN: "International Conference on Avian Tumor Viruses" (J.W. Beard ed.), pp. 277-298 (1964)], kindly provided by Jan Svoboda [Institute of Molecular Genetics, Czechoslovak Academy of Sciences; Prague, Czech Republic]; and

Rat 2-Tk$^-$ -- a thymidine kinase deficient cell line, kindly provided by L. Kutinova [Institute of Sera and Vaccines; Prague, Czech Republic]

CGL1	--	H/F-N hybrid cells (HeLa D98/AH.2 derivative)
CGL2	--	H/F-N hybrid cells (HeLa D98/AH.2 derivative)
CGL3	--	H/F-T hybrid cells (HeLa D98/AH.2 derivative)
CGL4	--	H/F-T hybrid cells (HeLa D98/Ah.2 derivative)

Nucleotide and Amino Acid Sequence Symbols

The following symbols are used to represent nucleotides herein:

Base Symbol	Meaning
A	adenine
C	cytosine
G	guanine
T	thymine
U	uracil
I	inosine
M	A or C
R	A or G
W	A or T/U
S	C or G
Y	C or T/U
K	G or T/U
V	A or C or G
H	A or C or T/U
D	A or G or T/U

B	C or G or T/U
N/X	A or C or G or T/U

There are twenty main amino acids, each of which is specified by a different arrangement of three adjacent nucleotides (triplet code or codon), and which are linked together in a specific order to form a characteristic protein. A three-letter or one-letter convention is used herein to identify said amino acids, as, for example, in Figure 1 as follows:

Amino acid name	3 Ltr. Abbrev.	1 Ltr. Abbrev.
Alanine	Ala	A
Arginine	Arg	R
Asparagine	Asn	N
Aspartic Acid	Asp	D
Cysteine	Cys	C
Glutamic Acid	Glu	E
Glutamine	Gln	Q
Glycine	Gly	G
Histidine	His	H
Isoleucine	Ile	I
Leucine	Leu	L
Lysine	Lys	K
Methionine	Met	M
Phenylalanine	Phe	F
Proline	Pro	P

Serine	Ser	S
Threonine	Thr	T
Tryptophan	Trp	W
Tyrosine	Tyr	Y
Valine	Val	V
Unknown or other		X

BRIEF DESCRIPTION OF THE FIGURES

Figure 1 provides the nucleotide sequence for a full-length MN cDNA [SEQ. ID. NO.: 1] clone isolated as described herein. Figure 1 also sets forth the predicted amino acid sequence [SEQ. ID. NO.: 2] encoded by the cDNA.

Figure 2 provides SDS-PAGE and immunoblotting analyses of recombinant MN protein expressed from a pGEX-3X bacterial expression vector. Two parallel samples of purified recombinant MN protein (twenty μg in each sample) were separated by SDS-PAGE on a 10% gel. One sample (A in Figure 2) was stained with Coomassie brilliant blue; whereas the other sample (B) was blotted onto a Hybond C membrane [Amersham; Aylesbury, Bucks, England]. The blot was developed by autoradiography with ^{125}I-labeled Mab M75.

Figure 3 illustrates inhibition of p54/58 expression by antisense oligodeoxynucleotides (ODNs). HeLa cells cultured in overcrowded conditions were incubated with (A) 29-mer ODNI [SEQ. ID. NO.: 3]; (B) 19-mer ODN2 [SEQ.

ID. NO.: 4]; (C) both ODNI and ODN2; and (D) without ODNS. Example 10 provides details of the procedures used.

Figure 4 shows the results of Northern blotting of MN mRNA in human cell lines. Total RNA was prepared from the following cell lines: HeLa cells growing in dense (A) and sparse (B) culture; (C) H/F-N; (D) and (E) H/F-T; and (F) human embryo fibroblasts. Example 11 details the procedure and results.

Figure 5 illustrates the detection of the MN gene in genomic DNAs by Southern blotting. Chromosomal DNA digested by PstI was as follows: (A) chicken; (B) bat; (C) rat; (D) mouse; (E) feline; (F) pig; (G) sheep; (H) bovine; (I) monkey; and (J) human HeLa cells. The procedures used are detailed in Example 12.

Figure 6 graphically illustrates the expression of MN- and MX-specific proteins in human fibroblasts (F), in HeLa cells (H) and in H/F-N and H/F-T hybrid cells and contrasts the expression in MX-infected and MX-uninfected cells. Example 5 details the procedures and results.

Figure 7 (discussed in Example 5) provides immunoblots of MN proteins in fibroblasts (FIBR) and in HeLa K, HeLa S, H/F-N and H/F-T hybrid cells.

Figure 8 (discussed in Example 6) shows immunoblots of MN proteins in cell culture extracts prepared from the following: (A) MX-infected HeLa cells; (B) human fibroblasts; (C) T24; (D) T47D; (E) SK-Mel 1477; and (F)

HeLa cells uninfected with MX. The symbols +ME and O ME indicate that the proteins were separated by PAGE after heating in a sample buffer, with and without 3% mercaptoethanol (ME), respectively.

Figure 9 (discussed in Example 6) provides immunoblots of MN proteins from human tissue extracts. The extracts were prepared from the following: (A) MX-infected HeLa cells; (B) full-term placenta; (C) corpus uteri; (D, M) adenocarcinoma endometrii; (E, N) carcinoma ovarii; (F, G) trophoblasts; (H) normal ovary; (I) myoma uteri; (J) mammary papilloma; (K) normal mammary gland; (L) hyperplastic endometrium; (O) cervical carcinoma; and (P) melanoma.

Figure 10 (discussed in Example 7) provides immunoblots of MN proteins from (A) MX-infected HeLa cells and from (B) Rat2-Tk$^-$cells. (+ME and 0 ME have the same meanings as explained in the legend to Figure 8.)

Figure 11 (discussed in Example 8) graphically illustrates the results from radioimmunoprecipitation experiments with ^{125}I-GEX-3X-MN protein and different antibodies. The radioactive protein (15 x 10^3 cpm/tube) was precipitated with ascitic fluid or sera and SAC as follows: (A) ascites with MAb M75; (B) rabbit anti-MaTu serum; (C) normal rabbit serum; (D) human serum L8; (E) human serum KH; and (F) human serum M7.

Figure 12 (discussed in Example 8) shows the results from radioimmunoassays for MN antigen. Ascitic

fluid (dilution precipitating 50% radioactivity) was allowed to react for 2 hours with (A) "cold" (unlabeled) protein GEX-3X-MN, or with extracts from cells as follows: (B) HeLa + MX; (C) Rat-2Tk$^-$; (D) HeLa; (E) rat XC; (F) T24; and (G) HEF. Subsequently ^{125}I-labeled GEX-3X-MN protein (25 x 10^3 cpm/tube) was added and incubated for an additional 2 hours. Finally, the radioactivity to MAb M75 was adsorbed to SAC and measured.

Figure 13 (discussed in Example 9) provides results of immunoelectron and scanning microscopy of MX-uninfected (control) and MX-infected HeLa cells. Panels A-D show ultrathin sections of cells stained with MAb M75 and immunogold; Panels E and F are scanning electron micrographs of cells wherein no immunogold was used. Panels E and F both show a terminal phase of cell division. Panels A and E are of control HeLa cells; panels B, C, D and F are of MX-infected HeLa cells. The cells shown in Panels A, B and C were fixed and treated with M75 and immunogold before they were embedded and sectioned. Such a procedure allows for immunogold decoration only of cell surface antigens. The cells in Panel D were treated with M75 and immunogold only once they had been embedded and sectioned, and thus antigens inside the cells could also be decorated.

Figure 14 compares the results of immunizing baby rats to XC tumor cells with rat serum prepared against the fusion protein MN glutathione S-transferase (GEX-3X-MN) (the

IM group) with the results of immunizing baby rats with control rat sera (the C group). Each point on the graph represents the tumor weight of a tumor from one rat. Example 14 details those experiments.

Figure 15a-d provides a 10,898 bp complete genomic sequence of MN [SEQ. ID. NO.: 5]. The base count is as follows: 2654 A; 2739 C; 2645 G; and 2859 T. The 11 exons are shown in capital letters.

Figure 16 is a restriction map of the full-length MN cDNA. The open reading frame is shown as an open box. The thick lines below the restriction map illustrate the sizes and positions of two overlapping cDNA clones. The horizontal arrows indicate the positions of primers R1 [SEQ. ID. NO.: 7] and R2 [SEQ. ID. NO.: 8] used for the 5′ end RACE. Relevant restriction sites are BamHI (B), EcoRV (V), EcoRI (E), PstI (Ps), PvuII (Pv).

Figure 17 shows a restriction analysis of the MN gene. Genomic DNA from HeLa cells was cleaved with the following restriction enzymes: EcoRI (1), EcoRV (2), HindIII (3), KpnI (4), NcoI (5), PstI (6), and PvuII (7), and then analyzed by Southern hybridization under stringent conditions using MN cDNA as a probe.

Figure 18 is a mapping of the transcription initiation (a) and termination (b) sites by RNase protection assay. MN-specific protected RNA fragments from CGL3 cells (2), HeLa (3) and HELA persistently infected with LCMV (4)

are indicated with arrows. NIH 3T3 cells (1) that do not express MN serve as a negative control.

Figure 19(a) shows an alignment of HCA plots derived from MN, human CA VI (hCA) and CA II (CA2). A one-letter code is used for all amino acids with exception of P (stars), G (diamond-shaped symbol), T and S (open and dotted squares, respectively). Strands D, E, F and G are essential for the structural core of CA. Topologically conserved hydrophobic amino acids are shaded (in hCA VI and MN). Ligands of the catalytic zinc ion (His residues) are indicated by arrowheads.

Figure 19(b) presents a stereoview of the CA II three-dimensional structure illustrating a superposition of the complete CA II structure (thin ribbon) with the structure which is well conserved in MN (open thick ribbon).

Figure 20 schematically represents the 5′ MN genomic region of an MN genomic clone.

Figure 21(a) shows the zinc-binding activity of MN protein extracted from HeLa cells persistently infected with LCMV. Samples were concentrated by immunoprecipitation with Mab M75 before loading (A), and after elution from $ZnCl_2$-saturated (B) or $ZnCl_2$-free Fast-Flow chelating Sepharase column (c). Immunoprecipitates were analyzed by Western blotting using iodinated M75 antibody.

Figure 21(b) shows MN protein binding to DNA-cellulose. Proteins extracted from LCMV-infected HeLa cells

were incubated with DNA-cellulose (A). Proteins that bound to DNA-cellulose in the presence of $ZnCl_2$ and absence of DTT (B), in the presence of both $ZnCl_2$ and DTT (C), and in the absence of both $ZnCl_2$ and DTT (D) were eluted, and all samples were analyzed as above.

Figure 21(c) shows the results of endoglycosidase H and F digestion. MN protein immunoprecipitated with Mab M75 was treated with Endo F (F) and Endo H (H). Treated (+) and control samples (-) were analyzed by Western blotting as above.

Figure 22 shows the morphology and growth kinetics of control (a, c, e and g) and MN-expressing (b, d, f and h) NIH 3T3 cells. The micrographs are of methanol fixed and Giemsa stained cells at a magnification X 100. Cells were grown to confluency (a, b), or as individual colonies in Petri dishes (c, d) and in soft agar (e, f). The (g) and (h) graphs provide growth curves of cells cultured in DMEM medium containing respectively, 10% and 1% FCS. The mean values of triplicate determinations were plotted against time.

Figure 23 illustrates flow cytometric analyses of asynchronous cell populations of control and MN cDNA-transfected NIH 3T3 cells.

Figure 24 is a map of the human MN gene. The numbered black boxes represent exons. The box designated

LTR denotes a region of homology to HERV-K LTR. The empty boxes are Alu-related sequences.

Figure 25 is a nucleotide sequence for the proposed promoter of the human MN gene [SEQ. ID. No.: 27]. The nucleotides are numbered from the transcription initiation site according to RNase protection assay. Potential regulatory elements are overlined. Transcription start sites are indicated by asterisks (RNase protection) and dots (RACE). The sequence of the 1st exon begins under the asterisks.

Figure 26 shows a CpG-rich island of a human MN gene. Each vertical line on the scale represents a CpG doublet (upper map) or a GpC doublet (lower map). CpG is 4-5 fold deficient in comparison to GpC, except the island region where the frequency increases about 5 time. CPG and GpC frequencies are roughly equal in the island region.

Figure 27 provides a schematic of the alignment of MN genomic clones according to their position related to the transcription initiation site. All the genomic fragments except Bd3 were isolated from a lambda FIX III genomic library derived from HeLa cells. Clone Bd3 was derived from a human fetal brain library.

Figure 28 shows the construction and cloning of a series of 5' deletion mutants of MN's putative promoter region linked to the bacterial CAT gene.

Figure 29 outlines the structure of MN promoter-CAT constructs.

DETAILED DESCRIPTION

As demonstrated herein MaTu was found to be a two-component system. One part of the complex, exogenous MX, is transmissible, and is manifested by a protein, p58X, which is a cytoplasmic antigen which reacts with some natural sera, of humans and of various animals. The other component, MN, is endogenous to human cells. The level of MN expression has been found to be considerably increased in the presence of the MaTu-MX transmissible agent, which has been now identified as lymphocytic choriomeningitis virus (LCMV) which persistently infects HeLa cells.

MN is a cellular gene, showing only very little homology with known DNA sequences. It is rather conservative and is present as a single copy gene in the chromosomal DNA of various vertebrates. The MN gene is shown herein to be organized into 11 exons and 10 introns. Described herein is the cloning and sequencing of the MN cDNA and genomic sequences, and the genetic engineering of MN proteins -- such as the GEX-3X-MN, MN-PA, MN-Fc and MN 20-19 proteins. The recombinant MN proteins can be conveniently purified by affinity chromatography.

MN is manifested in HeLa cells by a twin protein, p54/58N, that is localized on the cell surface and in the

nucleus. Immunoblots using a monoclonal antibody reactive with p54/58N (MAb M75) revealed two bands at 54 kd and 58 kd. Those two bands may correspond to one type of protein that differs by glycosylation pattern or by how it is processed. (Both p54N and p58N are glycosylated with oligosaccharidic residues containing mannose, but only p58N also contains glucosamine.) Herein, the phrase "twin protein" indicates p54/58N.

MN is absent in rapidly growing, sparse cultures of HeLa, but is inducible either by keeping the cells in dense cultures or, more efficiently, by infecting them with MX (LCMV). Those inducing factors are synergistic. p54/58N and not p58X is associated with virions of vesicular stomatitis virus (VSV), reproduced in MaTu-infected HeLa. Whereas the twin protein p54/58N is glycosylated and forms oligomers linked by disulfidic bonds, p58X is not glycosylated and does not form S-S-linked oligomers.

VSV assembles p54/58N into virions in HeLa cells, indicating that the twin protein is responsible for complementation of VSV G-protein mutants and for formation of VSV(MaTu) pseudotypes. As only enveloped viruses provide surface glycoproteins for the formation of infectious, functioning pseudotypes, which can perform such specific functions as adsorption and penetration of virions into cells [Zavada, J., J. Gen. Virol., 63: 15-24 (1982)], that

observation implies that the MN gene behaves as a quasi-viral sequence.

The surface proteins of enveloped viruses, which participate in the formation of VSV pseudotypes, are glycosylated as is the MN twin protein, p54/58N. MN proteins also resemble viral glycoproteins in the formation of oligomers (preferably tri- or tetramers); such oligomerization, although not necessarily involving S-S bonds (disulfidic bonds), is essential for the assembly of virions [Kreis and Lodish, Cell, 46: 929-937 (1986)]. The disulfidic bonds can be disrupted by reduction with 2-mercaptoethanol.

As reported in Pastorekova et al., Virology, 187: 620-626 (1992), after reduction with mercaptoethanol, p54/58N from cell extracts or from VSV looks very similar on immunoblot. Without reduction, in cell extracts, it gives several bands around 150 kd, suggesting that the cells may contain several different oligomers (probably with a different p54:p58 ratio), but VSV selectively assembles only one of them, with a molecular weight of about 153 kd. That oligomer might be a trimer, or rather a tetramer, consisting of 54 kd and 58 kd proteins. The equimolar ratio of p54:p58 in VSV virions is indicated by approximately the same strength of 54 kd and 58 kd bands in a VSV sample analyzed under reducing conditions.

The expression of MN proteins appears to be diagnostic/prognostic for neoplastic disease. The MN twin protein, p54/58N, was found to be expressed in HeLa cells and in Stanbridge's tumorigenic (H/F-T) hybrid cells [Stanbridge et al., Somatic Cell Genet, 7: 699-712 (1981); and Stanbridge et al., Science, 215: 252-259 (1982)] but not in fibroblasts or in non-tumorigenic (H/F-N) hybrid cells [Stanbridge et al., id.]. In early studies, MN proteins were found in immunoblots prepared from human ovarian, endometrial and uterine cervical carcinomas, and in some benign neoplasias (as mammary papilloma) but not from normal ovarian, endometrial, uterine or placental tissues. Example 13 details further research on MN gene expression wherein MN antigen, as detected by immunohistochemical staining, was found to be prevalent in tumor cells of a number of cancers, including cervical, bladder, head and neck, and renal cell carcinomas among others. Further, the immunohistochemical staining experiments of Example 13 show that among normal tissues tested, only normal stomach tissues showed routinely and extensively the presence of MN antigen. MN antigen is further shown herein to be present sometimes in morphologically normal-appearing areas of tissue specimens exhibiting dysplasia and/or malignancy.

In HeLa cells infected with MX, observed were conspicuous ultrastructural alterations, that is, the formation of abundant filaments on cell surfaces and the

amplification of mitochondria. Using an immunogold technique, p54/58N was visualized on the surface filaments and in the nucleus, particularly in the nucleoli. Thus MN proteins appear to be strongly correlated with tumorigenicity, and do not appear to be produced in general by normal non-tumor cells.

Examples herein show that MX and MN are two different entities, that can exist independently of each other. MX (LCMV) as an exogenous, transmissible agent can multiply in fibroblasts and in H/F-N hybrid cells which are not expressing MN-related proteins (Figure 6). In such cells, MX does not induce the production of MN protein. MN protein can be produced in HeLa and other tumor cells even in the absence of MX as shown in Figures 6-9. However, MX is a potent inducer of MN-related protein in HeLa cells; it increases its production thirty times over the concentration observed in uninfected cells (Figures 7 and 12, Table 2 in Example 8, below).

MN Gene--Cloning and Sequencing

Figure 1 provides the nucleotide sequence for a full-length MN cDNA clone isolated as described below [SEQ. ID. NO.: 1]. Figure 15a-d provides a complete MN genomic sequence [SEQ. ID. NO.: 5]. Figure 25 shows the nucleotide sequence for a proposed MN promoter [SEQ. ID. NO.: 27].

It is understood that because of the degeneracy of the genetic code, that is, that more than one codon will code for one amino acid [for example, the codons TTA, TTG, CTT, CTC, CTA and CTG each code for the amino acid leucine (leu)], that variations of the nucleotide sequences in, for example, SEQ. ID. NOS.: 1 and 5 wherein one codon is substituted for another, would produce a substantially equivalent protein or polypeptide according to this invention. All such variations in the nucleotide sequences of the MN cDNA and complementary nucleic acid sequences are included within the scope of this invention.

It is further understood that the nucleotide sequences herein described and shown in Figures 1, 15a-d and 25, represent only the precise structures of the cDNA, genomic and promoter nucleotide sequences isolated and described herein. It is expected that slightly modified nucleotide sequences will be found or can be modified by techniques known in the art to code for substantially similar or homologous MN proteins and polypeptides, for example, those having similar epitopes, and such nucleotide sequences and proteins/polypeptides are considered to be equivalents for the purpose of this invention. DNA or RNA having equivalent codons is considered within the scope of the invention, as are synthetic nucleic acid sequences that encode proteins/polypeptides homologous or substantially homologous to MN proteins/polypeptides, as well as those

nucleic acid sequences that would hybridize to said exemplary sequences [SEQ. ID. NOS. 1, 5 and 27] under stringent conditions or that but for the degeneracy of the genetic code would hybridize to said cDNA nucleotide sequences under stringent hybridization conditions. Modifications and variations of nucleic acid sequences as indicated herein are considered to result in sequences that are substantially the same as the exemplary MN sequences and fragments thereof.

Partial cDNA clone

To find the MN gene, a lambda gt11 cDNA library from MX-infected HeLa cells was prepared. Total RNA from MX-infected HeLa cells was isolated by a guanidinium-thiocyanate-CsCl method [Chirgwin et al., Biochemistry, 18: 5249 (1979)], and the mRNA was affinity separated on oligo dT-cellulose [Ausubel et al., Short Protocols in Molecular Biology, (Greene Publishing Assocs. and Wiley-Interscience; NY, USA, 1989]. The synthesis of the cDNA and its cloning into lambda gt11 was carried out using kits from Amersham, except that the EcoRI-NotI adaptor was from Stratagene [La Jolla, CA (USA)]. The library was subjected to immunoscreening with Mab M75 in combination with goat anti-mouse antibodies conjugated with alkaline phosphatase. That immunoscreening method is described in Young and Davis, PNAS (USA), 80: 1194-1198 (1983). About 4 x 10^5 primary plaques

on E. coli Y1090 cells, representing about one-half of the whole library, were screened using Hybond N+ membrane [Amersham] saturated with 10 mM IPTG and blocked with 5% FCS. Fusion proteins were detected with Mab M75 in combination with goat anti-mouse antibodies conjugated with alkaline phosphatase. One positive clone was picked.

pBluescript-MN. The positive clone was subcloned into the NotI site of pBluescript KS [Stratagene] thereby creating pBluescript-MN. Two oppositely oriented nested deletions were made using Erase-a-Base™ kit [Promega; Madison, WI (USA)] and sequenced by dideoxy method with a T7 sequencing kit [Pharmacia; Piscataway, NJ (USA)]. The sequencing showed a partial cDNA clone, the insert being 1397 bp long. The sequence comprises a large 1290 bp open reading frame and 107 bp 3′ untranslated region containing a polyadenylation signal (AATAAA). Another interesting feature of the sequence is the presence of a region contributing to instability of the mRNA (AUUUA at position 1389) which is characteristic for mRNAs of some oncogenes and lymphokines [Shaw and Kamen, Cell, 46: 659-667 (1986)]. However, the sequence surrounding the first ATG codon in the open reading frame (ORF) did not fit the definition of a translational start site. In addition, as follows from a comparison of the size of the MN clone with that of the corresponding mRNA in a Northern blot (Figure 4), the cDNA was missing about 100 bp from the 5′ end of its sequence.

Full-Length cDNA Clone

Attempts to isolate a full-length clone from the original cDNA library failed. Therefore, we performed a rapid amplification of cDNA ends (RACE) using MN-specific primers, R1 and R2, derived from the 5′ region of the original cDNA clone. The RACE product was inserted into pBluescript, and the entire population of recombinant plasmids was sequenced with an MN-specific primer ODN1. In that way, we obtained a reliable sequence at the very 5′ end of the MN cDNA as shown in Figure 1 [SEQ. ID. NO.: 1].

Specifically, RACE was performed using 5′ RACE System [GIBCO BRL; Gaithersburg, MD (USA)] as follows. 1 μg of mRNA (the same as above) was used as a template for the first strand cDNA synthesis which was primed by the MN-specific antisense oligonucleotide, R1 (5′-TGGGGTTCTTGAGGATCTCCAGGAG-3′) [SEQ. ID. NO.: 7]. The first strand product was precipitated twice in the presence of ammonium acetate and a homopolymeric C tail was attached to its 3′ end by TdT. Tailed cDNA was then amplified by PCR using a nested primer, R2 (5′-CTCTAACTTCAGGGAGCCCTCTTCTT-3′) [SEQ. ID. NO.: 8] and an anchor primer that anneals to the homopolymeric tail (5′-CUACUACUACUAGGCCACGCGTCGACTAGTACGGGI IGGGIIGGGIIG-3′) [SEQ. ID. NO.: 9]. Amplified product was digested with BamHI and SalI restriction enzymes and cloned into pBluescript II KS plasmid. After transformation, plasmid DNA was purified from the whole population of

transformed cells and used as a template for the sequencing with the MN-specific primer ODN1 [SEQ. ID. NO.: 3; a 29-mer, the sequence for which is shown in Example 10].

Based upon results of the RACE analysis, the full-length MN cDNA sequence was seen to contain a single ORF starting at position 12, with an ATG codon that is in a good context (GCGCATGG) with the rule proposed for translation initiation [Kozak, J. Cell. Biol., 108: 229-241 (1989)]. [See below under Mapping of MN Gene Transcription Initiation Site for fine mapping of the 5′ end of the MN gene.] The AT rich 3′ untranslated region contains a polyadenylation signal (AATAAA) preceding the end of the cDNA by 10 bp. Surprisingly, the sequence from the original clone as well as from four additional clones obtained from the same cDNA library did not reveal any poly(A) tail. Moreover, as indicated above, just downstream of the poly(A) signal we found an ATTTA motif that is thought to contribute to mRNA instability (Shaw and Kamen, supra). This fact raised the possibility that the poly (A) tail is missing due to the specific degradation of the MN mRNA.

Genomic clones

To study MN regulation, MN genomic clones were isolated. One MN genomic clone (Bd3) was isolated from a human cosmid library prepared from fetal brain using both the MN cDNA probe and the MN-specific primers derived from

the 5′ end of the cDNA [SEQ. ID. NOS.: 3 and 4; ODN1 AND ODN2; see Example 10]. Sequence analysis revealed that that genomic clone covers a region upstream from a MN transcription start site and ending with the BamHI restriction site localized inside the MN cDNA. Other MN genomic clones can be similarly isolated.

In order to identify the complete genomic region of MN, the human genomic library in Lambda FIX II vector (Stratagene) was prepared from HeLa chromosomal DNA and screened by plaque hybridization using the MN cDNA as described below. Several independent MN recombinant phages were identified, isolated and characterized by restriction mapping and hybridization analyses. Four overlapping recombinants covering the whole genomic region of MN were selected, digested and subcloned into pBluescript. The subclones were then subjected to bidirectional nested deletions and sequencing. DNA sequences were compiled and analyzed by computer using the DNASIS software package.

The details of isolating genomic clones covering the complete genomic region for MN are provided below. Figure 27 provides a schematic of the alignment of MN genomic clones according to the transcription initiation site. Plasmids containing the A4a clone and the XE1 and XE3 subclones were deposited at the American Type Culture Collection (ATCC) at 12301 Parklawn Drive, Rockville, MD

20852 (USA) on June ___, 1995, respectively under ATCC Deposit Nos. _____, _____, and _____.

Isolation of Genomic DNA Clones

The Sau3AI human HeLa genomic library was prepared in Lambda FIX II vector [Stratagene; La Jolla, CA (USA)] according to manufacturer's protocol. Human fetal brain cosmid library in SuperCos cosmid was from Stratagene. Recombinant phages or bacteria were plated at 1 x 10^5 plaque forming units on 22x22 cm Nunc plates or 5 x 10^4 cells on 150 mm Petri dishes, and plaques or colonies were transferred to Hybond N membranes (Amersham). Hybridization was carried out with the full-length MN cDNA labeled with [P^{32}]PdCTP by the Multiprime DNA labeling method (Amersham) at 65°C in 6 x SSC, 0.5% SDS, 10 x Denhardt's and 0.2 mg/1 ml salmon sperm DNA. Filters were washed twice in 2 x SSC, 0.1% SDS at 65°C for 20 min. The dried filters were exposed to X-ray films, and positive clones were picked up. Phages and bacteria were isolated by 3-4 sequential rounds of screening.

Subcloning and DNA Sequencing

Genomic DNA fragments were subcloned into a pBluescript KS and templates for sequencing were generated by serial nested deletions using Erase-a-Base system (Promega). Sequencing was performed by the

dideoxynucleotide chain termination method using T7 sequencing kit (Pharmacia). Nucleotide sequence alignments and analyses were carried out using the DNASIS software package (Hitachi Software Engineering).

Exon-Intron Structure of Complete MN Genomic Region

The complete sequence of the overlapping clones contains 10,898 bp (SEQ. ID. NO.: 5). Figure 24 depicts the organization of the human MN gene, showing the location of all 11 exons as well as the 2 upstream and 6 intronic Alu repeat elements. All the exons are small, ranging from 27 to 191 bp, with the exception of the first exon which is 445 bp. The intron sizes range from 89 to 1400 bp.

Table 1 below lists the splice donor and acceptor sequences that conform to consensus splice sequences including the AG-GT motif [Mount, "A catalogue of splice junction sequences," Nucleic Acids Res. 10: 459-472 (1982)].

TABLE 1
Exon-Intron Structure of the Human MN Gene

Exon	Size	Genomic Position**	SEQ ID NO	5'splice donor	SEQ ID No
1	445	*3507-3951	28	AGAAG gtaagt	67
2	30	5126-5155	29	TGGAG gtgaga	68
3	171	5349-5519	30	CAGTC gtgagg	69
4	143	5651-5793	31	CCGAG gtgagc	70
5	93	5883-5975	32	TGGAG gtacca	71
6	67	7376-7442	33	GGAAG gtcagt	72
7	158	8777-8934	34	AGCAG gtgggc	73
8	145	9447-9591	35	GCCAG gtacag	74
9	27	9706-9732	36	TGCTG gtgagt	75
10	82	10350-10431	37	CACAG gtatta	76
11	191	10562-10752	38	ATAAT end	

Intron	Size	Genomic Position**	SEQ ID NO	3'splice acceptor	SEQ ID NO
1	1174	3952-5125	39	atacag GGGAT	77
2	193	5156-5348	40	ccccag GCGAC	78
3	131	5520-5650	41	acgcag TGCAA	79
4	89	5794-5882	42	tttcag ATCCA	80
5	1400	5976-7375	43	ccccag GAGGG	81
6	1334	7443-8776	44	tcacag GCTCA	82
7	512	8935-9446	45	ccctag CTCCA	83
8	114	9592-9705	46	ctccag TCCAG	84
9	617	9733-10349	47	tcgcag GTGACA	85
10	130	10432-10561	48	acacag AAGGG	86

** positions are related to nt numbering in whole genomic sequence including the 5' flanking region [Figure 15a-d]
* number corresponds to transcription initiation site determined below by RNase protection assay

A search for sequences related to MN gene in the EMBL Data Library did not reveal any specific homology except for 6 complete and 2 partial Alu-type repeats with homology to Alu sequences ranging from 69.8% to 91% [Jurka and Milosavljevic, "Reconstruction and analysis of human Alu genes," J. Mol. Evol. 32: 105-121 (1991)]. Below under the Characterization of the 5′ Flanking Region, also a 222 bp sequence proximal to the 5′ end of the genomic region is shown to be closely homologous to a region of the HERV-K LTR.

Mapping of MN Gene Transcription Initiation Site

In our earlier attempt to localize the site of transcription initiation of the MN gene by RACE (above), we obtained a major PCR fragment whose sequence placed the start site 12 bp upstream from the first codon of the ORF. That result was obtained probably due to a preferential amplification of the shortest form of mRNA. Therefore, we used an RNase protection assay (RNP) for fine mapping of the 5′ end of the MN gene. The probe was a uniformly labeled 470 nucleotide copy RNA (nt -205 to +265) [SEQ. ID. NO.: 55], which was hybridized to total RNA from MN-expressing HeLa and CGL3 cells and analyzed on a sequencing gel. That analysis has shown that the MN gene transcription initiates at multiple sites, the 5′ end of the longest MN transcript

being 30 nt longer than that previously characterized by RACE (Figure 18a).

RNase Protection Assay

^{32}P-labeled RNA probes were prepared with an RNA Transcription kit (Stratagene). In vitro transcription reactions were carried out using 1 μg of the linearized plasmid as a template, 50 μCi of [P^{32}P]rUTP (800 Ci/mmol), 10 U of either T3 or T7 RNA polymerase and other components of the Transcription Kit following instructions of the supplier. For mapping of the 5′ end of MN mRNA, 470 bp NcoI-BamHI fragment (NcoI filled in by Klenow enzyme) of Bd3 clone (nt -205 to +265 related to transcription start) was subcloned to EcoRV-BamHI sites of pBluescript SK+, linearized with HindIII and labeled with T3 RNA polymerase. For the 3′ end mRNA analysis, probe, that was prepared using T7 RNA polymerase on KS-dXE3-16 template (one of the nested deletion clones of MN genomic region XE3 subclone) digested with Sau3AI (which cuts exon 11 at position 10,629), was used. Approximately 3 x 10^5 cpm of RNA probe were used per one RNase protection assay reaction.

RNase protection assays (RNP) were performed using Lysate RNase Protection Kit (USB/Amersham) according to protocols of the supplier. Briefly, cells were lysed using Lysis Solution at concentration of approximately 107 cells/ml, and 45 μ1 of the cell homogenate were used in

RNA/RNA hybridization reactions with ^{32}P-labeled RNA probes prepared as described above. Following overnight hybridizations at 42°C, homogenates were treated for 30 min at 37°C with RNase cocktail mix. Protected RNA duplexes were run on polyacrylamide/urea denaturing sequencing gels. Fixed and dried gels were exposed to X-ray film for 24 - 72 hours.

Mapping of MN Gene Transcription Termination Site

An RNase protection assay, as described above, was also used to verify also the 3′ end of the MN cDNA. That was important with respect to our previous finding that the cDNA contains a poly(A) signal but lacks a poly(A) tail, which could be lost during the proposed degradation of MN mRNA due to the presence of an instability motif in its 3′ untranslated region. RNP analysis of MN mRNA with the fragment of the genomic clone XE3 covering the region of interest corroborated our data from MN cDNA sequencing, since the 3′ end of the protected fragment corresponded to the last base of MN cDNA (position 10,752 of the genomic sequence). That site also meets the requirement for the presence of a second signal in the genomic sequence that is needed for transcription termination and polyadenylation [McLauchlan et al., Nucleic Acids Res., 13: 1347 (1985)]. Motif TGTGTTAGT (nt 10,759-10,767) corresponds well to both the consensus sequence and the position of that signal

within 22 bp downstream from the polyA signal (nt 10,737-10,742).

Characterization of the 5′ Flanking Region

The Bd3 genomic clone isolated from human fetal brain cosmid library was found to cover a region of 3.5 kb upstream from the transcription start site of the MN gene. It contains no significant coding region. Two Alu repeats are situated at positions -2587 to -2296 [SEQ. ID. NO.: 56] and -1138 to -877 [SEQ. ID. NO.: 57] (with respect to the transcription start determined by RNP). The sequence proximal to the 5′ end is strongly homologous (91.4% identity) to the U3 region of long terminal repeats of human endogenous retroviruses HERV-K [Ono, M., "Molecular cloning and long terminal repeat sequences of human endogenous retrovirus genes related to types A and B retrovirus genes," J. Virol, 58: 937-944 (1986)]. The LTR-like fragment is 222 bp long with an A-rich tail at its 3′ end. Most probably, it represents part of SINE (short interspersed repeated sequence) type nonviral retroposon derived from HERV-K [Ono et al., "A novel human nonviral retroposon derived from an endogenous retrovirus," Nucleic Acids Res., 15: 8725-8373 (1987)]. There are no sequences corresponding to regulatory elements in this fragment, since the 3′ part of U3, and the entire R and U5 regions of LTR are absent from the Bd3 genomic clone, and the

glucocorticoid responsive element as well as the enhancer core sequences are beyond its 5′ border.

However, two keratinocyte-dependent enhancers were identified in the sequence downstream from the LTR-like fragment at positions -3010 and -2814. Those elements are involved in transcriptional regulation of the E6-E7 oncogenes of human papillomaviruses and are thought to account for their tissue specificity [Cripe et al., "Transcriptional regulation of the human papilloma-virus-16 E6-E7 promoter by a keratinocyte-dependent enhancer, and by viral E2 trans-activator and repressor gene products: implications for cervical carcinogenesis," EMBO J., 6: 3745-3753 (1987)].

Nucleotide sequence analysis of the DNA 5′ to the transcription start (from nt -507) revealed no recognizable TATA box within the expected distance from the beginning of the first exon (Figure 25). However, the presence of potential binding sites for transcription factors suggests that this region might contain a promoter for the MN gene. There are several consensus sequences for transcription factors AP1 and AP2 as well as for other regulatory elements, including a p53 binding site [Locker and Buzard, "A dictionary of transcription control sequences," J. DNA Sequencing and Mapping, 1: 3-11 (1990); Imagawa et al., "Transcription factor AP-2 mediates induction by two different signal-transduction pathways: protein kinase C

and cAMP," Cell, 51: 251-260 (1987); El Deiry et al., "Human genomic DNA sequences define a consensus binding site for p53," Nat. Genet., 1: 44-49 (1992)]. Although the putative promoter region contains 59.3% C+G, it does not have additional attributes of CpG-rich islands that are typical for TATA-less promoters of housekeeping genes [Bird, "CPG-rich islands and the function of DNA methylation," Nature, 321: 209-213 (1986)]. Another class of genes lacking TATA box utilizes the initiator (Inr) element as a promoter. Many of these genes are not constitutively active, but they are rather regulated during differentiation or development. The Inr has a consensus sequence of PyPyPyCAPyPyPyPyPy [SEQ. ID. NO.: 23] and encompasses the transcription start site [Smale and Baltimore, "The 'initiator' as a transcription control element," Cell, 57: 103-113 (1989)]. There are two such consensus sequences in the MN putative promoter; however, they do not overlap the transcription start (Figure 25).

In the initial experiments, we were unable to show promoter activity in human carcinoma cells HeLa and CGL3 that express MN, using the 3.5 kb Bd3 fragment and series of its deletion mutants (from nt -933 to -30) [SEQ. ID. NO.: 58] fused to chloramphenicol acetyl transferase (CAT) gene in a transient system. This might indicate that either the promoter activity of the region 5' to the MN transcription start is below the sensitivity of the CAT assay, or

additional regulatory elements not present in our constructs are required for driving the expression of MN gene.

With respect to this fact, an interesting region was found in the middle of the MN gene. The region is about 1.4 kb in length [nt 4,600-6,000 of the genomic sequence; SEQ. ID. NO.: 49] and spans from the 3′ part of the 1st intron to the end of the 5th exon. The region has the character of a typical CpG-rich island, with 62.8% C+G content and 82 CpG: 131 GpC dinucleotides (Figure 26). Moreover, there are multiple putative binding sites for transcription factors AP2 and Sp1 [Locker and Buzard, supra; Briggs et al., "Purification and biochemical characterization of the promoter-specific transcription factor Sp-1," Science, 234: 47-52 (1986)] concentrated in the center of this area. Particularly the 3rd intron of 131 bp in length contains three Sp1 and three AP2 consensus sequences. That data indicates the possible involvement of that region in the regulation of MN gene expression. However, functionality of that region, as well as other regulatory elements found in the proposed 5′ MN promoter, remains to be determined.

MN Promoter Analysis

To define sequences necessary for MN gene expression, a series of 5′ deletion mutants of the putative promoter region were fused to the bacterial chloramphenicol

acetyltransferase (CAT) gene. [See Figures 28 and 29.] The pMN-CAT deletion constructs were transfected using a DEAE dextran method for transient expression into HeLa and CGL3 cells. Those cells were used since they naturally express MN protein, and thus, should contain all the required transcription factors.

After 48 hours, crude cell lysates were prepared and the activity of the expressed CAT was evaluated according to acetylation of [^{14}C]chloramphenicol by thin layer chromatography. However, no MN promoter CAT activity was detected in either the HeLa or the CGL3 cells in a transient system. On the other hand, reporter CAT plasmids with viral promoters (e.g. pBLV-LTR + tax transactivator, pRSV CAT and pSV2 CAT), that served as positive controls, gave strong signals on the chromatogram. [pSV2 CAT carries the SV40 origin and expresses CAT from the SV40 early promoter (P_E). pRSV CAT expresses CAT from the Rous sarcoma virus (RSV)LTR promoter (P_{LTR}).]

No detectable CAT activity was observed in additional experiments using increasing amounts of transfected plasmids (from 2 to 20 g DNA per dish) and prolonged periods of cell incubation after transcription. Increased cell density also did not improve the results (in contrast to the expectations based on density-dependent expression of native MN protein in HeLa cells). Since we found consensus sequences for transcription factors AP2 and

AP1 in the putative MN promoter, we studied the effect of their inducers dexamethasone (1 m) and phorbol ester phorbol 12-myristate 13-acetate (PMA 50 ng/ml) on CAT activity. However, the MN promoter was unresponsive to those compounds.

The following provides explanations for the results:

-- the putative MN promoter immediately preceding the transcription initiation site is very weak, and its activity is below the sensitivity of a standard CAT assay;

-- additional sequences (e.g enhancers) are necessary for MN transcription.

To further shed light on the regulation of MN expression at the level of transcription, constructs, analogously prepared to the MN-CAT constructs, are prepared, wherein the MN promoter region is upstream from the neomycin phosphotransferase gene engineered for mammalian expression. Such constructs are then transfected to cells which are subjected to selection with G418. Activity of the promoter is then evaluated on the basis of the number of G418 resistant colonies that result. That method has the capacity to detect activity of a promoter that is 50 to 100 times weaker in comparison to promoters detectable by a CAT assay.

Deduced Amino Acid Sequence

The ORF of the MN cDNA shown in Figure 1 has the coding capacity for a 459 amino acid protein with a calculated molecular weight of 49.7 kd. MN protein has an estimated pI of about 4. As assessed by amino acid sequence analysis, the deduced primary structure of the MN protein can be divided into four distinct regions. The initial hydrophobic region of 37 amino acids (AA) corresponds to a signal peptide. The mature protein has an N-terminal part of 377 AA, a hydrophobic transmembrane segment of 20 AA and a C-terminal region of 25 AA. Alternatively, the MN protein can be viewed as having five domains as follows: (1) a signal peptide [amino acids (AA) 1-37; SEQ. ID. NO.: 6]; (2) a region of homology to collagen alpha1 chain (AA 38-135; SEQ. ID. NO.: 50); (3) a carbonic anhydrase domain (AA 136-391; SEQ. ID. NO.: 51); (4) a transmembrane region (AA 414-433; SEQ. ID. NO.: 52); and (5) an intracellular C terminus (AA 435-459; SEQ. ID. NO.: 53). (The AA numbers are keyed to Figure 1.)

More detailed insight into MN protein primary structure disclosed the presence of several consensus sequences. One potential N-glycosylation site was found at position 346 of Figure 1. That feature, together with a predicted membrane-spanning region are consistent with the results, in which MN was shown to be an N-glycosylated protein localized in the plasma membrane. MN protein

sequence deduced from cDNA was also found to contain seven S/TPXX sequence elements [SEQ. ID. NOS.: 25 AND 26] (one of them is in the signal peptide) defined by Suzuki, J. Mol. Biol., 207: 61-84 (1989) as motifs frequently found in gene regulatory proteins. However, only two of them are composed of the suggested consensus amino acids.

In experiments, the results for which are shown in Figure 21(a), it was determined that MN protein is able to bind zinc cations, as shown by affinity chromatography using Zn-charged chelating sepharose. MN protein immunoprecipitated from HeLa cells by Mab M75 was found to have weak catalytic activity of CA. The CA-like domain of MN has a structural predisposition to serve as a binding site for small soluble domains. Thus, MN protein could mediate some kind of signal transduction.

MN protein from LCMV-infected HeLA cells was shown by using DNA cellulose affinity chromatography [Figure 21(b)] to bind to immobilized double-stranded salmon sperm DNA. The binding activity required both the presence of zinc cations and the absence of a reducing agent in the binding buffer.

Sequence Similarities

Computer analysis of the MN cDNA sequence was carried out using DNASIS and PROSID (Pharmacia Software packages). GenBank, EMBL, Protein Identification Resource

and SWISS-PROT databases were searched for all possible sequence similarities. In addition, a search for proteins sharing sequence similarities with MN was performed in the MIPS databank with the FastA program [Pearson and Lipman, PNAS (USA), 85: 2444 (1988)].

The MN gene was found to clearly be a novel sequence derived from the human genome. Searches for amino acid sequence similarities in protein databases revealed as the closest homology a level of sequence identity (38.9% in 256 AA or 44% in an 170 AA overlap) between the central part of the MN protein [AAs 136-391 (SEQ. ID. NO: 51)] or 221-390 [SEQ. ID. NO.: 54] of Figure 1 and carbonic anhydrases (CA). However, the overall sequence homology between the cDNA MN sequence and cDNA sequences encoding different CA isoenzymes is in a homology range of 48-50% which is considered by ones in the art to be low. Therefore, the MN cDNA sequence is not closely related to any CA cDNA sequences.

Only very closely related nt sequences having a homology of at least 80-90% would hybridize to each other under stringent conditions. A sequence comparison of the MN cDNA sequence shown in Figure 1 and a corresponding cDNA of the human carbonic anhydrase II (CA II) showed that there are no stretches of identity between the two sequences that would be long enough to allow for a segment of the CA II cDNA sequence having 50 or more nucleotides to hybridize

under stringent hybridization conditions to the MN cDNA or vice versa.

Although MN deduced amino acid sequences show some homology to known carbonic anhydrases, they differ from them in several repects. Seven carbonic anhydrases are known [Dodgson et al. (eds.), The Carbonic Anhydrases, (Plenum Press; New York/London (1991)]. All of the known carbonic anhydrases are proteins of about 30 kd, smaller than the p54/58N-related products of the MN gene. Further, the carbonic anhydrases do not form oligomers as do the MN-related proteins.

The N-terminal part of the MN protein (AA 38-135; SEQ. ID. NO.: 50) shows a 27-30% identity with human collagen alpha1 chain, which is an important component of the extracellular matrix.

MN Twin Protein

The possibility that the 4 kd difference between the molecular weights of the two MN proteins is caused by different glycosylation was ruled out, since after in vitro treatment with endoglycosidases H and F, respectively, both peptide portions lost about 3 kd in weight. This result indicates, in addition, that the molecular weight of the smaller 54 kd MN protein without its 3 kd sugar moiety, roughly corresponds to the molecular weight of MN calculated from the full-length cDNA. Western blot analysis of MN

proteins from cervical carcinoma and normal stomach shows that in both tissues MN protein consists of two 54 and 58 kd peptide portions.

To determine whether both p54/58N proteins were encoded by one gene, antisense ODNs were used to inhibit specifically MN gene expression. [Such use of antisense ODNs is reviewed in Stein and Cohen, Cancer Res., 48: 2659-2668 (1988).] Those experiments are detailed in Example 10. The findings indicated that cultivation of HeLa cells with ODNs resulted in a considerable inhibition of p54/58N synthesis, whereas the amount of different HeLa cell proteins produced remained approximately the same. Further, and importantly, on immunoblotting, the specific inhibition by ODNs affected both of the p54/58N proteins (Figure 3). Thus, it was concluded that the MN gene that was cloned codes for both of the p54/58N proteins in HeLa cells.

MN Proteins and/or Polypeptides

The phrase "MN proteins and/or polypeptides" (MN proteins/polypeptides) is herein defined to mean proteins and/or polypeptides encoded by an MN gene or fragments thereof. An exemplary and preferred MN protein according to this invention has the deduced amino acid sequence shown in Figure 1. Preferred MN proteins/polypeptides are those proteins and/or polypeptides that have substantial homology with the MN protein shown in Figure 1. For example, such

substantially homologous MN proteins/ polypeptides are those that are reactive with the MN-specific antibodies of this invention, preferably the Mabs M75, MN12, MN9 and MN7 or their equivalents.

A "polypeptide" is a chain of amino acids covalently bound by peptide linkages and is herein considered to be composed of 50 or less amino acids. A "protein" is herein defined to be a polypeptide composed of more than 50 amino acids.

MN proteins exhibit several interesting features: cell membrane localization, cell density dependent expression in HeLa cells, correlation with the tumorigenic phenotype of HeLa x fibroblast somatic cell hybrids, and expression in several human carcinomas among other tissues. As demonstrated herein, for example, in Example 13, MN protein can be found directly in tumor tissue sections but not in general in counterpart normal tissues (exceptions noted infra in Example 13 as in normal stomach tissues). MN is also expressed sometimes in morphologically normal appearing areas of tissue specimens exhibiting dysplasia and/or malignancy. Taken together, these features suggest a possible involvement of MN in the regulation of cell proliferation, differentiation and/or transformation.

It can be appreciated that a protein or polypeptide produced by a neoplastic cell in vivo could be altered in sequence from that produced by a tumor cell in

cell culture or by a transformed cell. Thus, MN proteins and/or polypeptides which have varying amino acid sequences including without limitation, amino acid substitutions, extensions, deletions, truncations and combinations thereof, fall within the scope of this invention. It can also be appreciated that a protein extant within body fluids is subject to degradative processes, such as, proteolytic processes; thus, MN proteins that are significantly truncated and MN polypeptides may be found in body fluids, such as, sera. The phrase "MN antigen" is used herein to encompass MN proteins and/or polypeptides.

It will further be appreciated that the amino acid sequence of MN proteins and polypeptides can be modified by genetic techniques. One or more amino acids can be deleted or substituted. Such amino acid changes may not cause any measurable change in the biological activity of the protein or polypeptide and result in proteins or polypeptides which are within the scope of this invention, as well as, MN muteins.

The MN proteins and polypeptides of this invention can be prepared in a variety of ways according to this invention, for example, recombinantly, synthetically or otherwise biologically, that is, by cleaving longer proteins and polypeptides enzymatically and/or chemically. A preferred method to prepare MN proteins is by a recombinant means. Particularly preferred methods of recombinantly

producing MN proteins are described below for the GEX-3X-MN, MN 20-19, MN-Fc and MN-PA proteins.

Recombinant Production of MN Proteins and Polypeptides

A representative method to prepare the MN proteins shown in Figure 1 or fragments thereof would be to insert the full-length or an appropriate fragment of MN cDNA into an appropriate expression vector as exemplified below. The fusion protein GEX-3X-MN expressed from XL1-Blue cells is nonglycosylated. Representative of a glycosylated, recombinantly produced MN protein is the MN 20-19 protein expressed from insect cells. The MN 20-19 protein was also expressed in a nonglycosylated form in E. coli using the expression plasmid pEt-22b [Novagen].

Baculovirus Expression Systems. Recombinant baculovirus express vectors have been developed for infection into several types of insect cells. For example, recombinant baculoviruses have been developed for among others: Aedes aegypti, Autographa californica, Bombyx mor, Drosphila melanogaster, Heliothis zea, Spodoptera frugiperda, and Trichoplusia ni [PCT Pub. No. WO 89/046699; Wright, Nature, 321: 718 (1986); Fraser et al., In Vitro Cell Dev. Biol., 25: 225 (1989). Methods of introducing exogenous DNA into insect hosts are well-known in the art. DNA transfection and viral infection procedures usually vary with the insect genus to be transformed. See, for example,

Autographa [Carstens et al., Virology, 101: 311 (1980)]; Spodoptera [Kang, "Baculovirus Vectors for Expression of Foreign Genes," in: Advances in Virus Research, 35 (1988)]; and Heliothis (virescens) [PCT Pub. No. WO 88/02030].

A wide variety of other host-cloning vector combinations may be usefully employed in cloning the MN DNA isolated as described herein. For example, useful cloning vehicles may include chromosomal, nonchromosomal and synthetic DNA sequences such as various known bacterial plasmids such as pBR322, other E. coli plasmids and their derivatives and wider host range plasmids such as RP4, phage DNA, such as, the numerous derivatives of phage lambda, e.g., NB989 and vectors derived from combinations of plasmids and phage DNAs such as plasmids which have been modified to employ phage DNA expression control sequences.

Useful hosts may be eukaryotic or prokaryotic and include bacterial hosts such as E. coli and other bacterial strains, yeasts and other fungi, animal or plant hosts such as animal or plant cells in culture, insect cells and other hosts. Of course, not all hosts may be equally efficient. The particular selection of host-cloning vehicle combination may be made by those of skill in the art after due consideration of the principles set forth herein without departing from the scope of this invention.

The particular site chosen for insertion of the selected DNA fragment into the cloning vehicle to form a

recombinant DNA molecule is determined by a variety of factors. These include size and structure of the protein or polypeptide to be expressed, susceptibility of the desired protein or polypeptide to endoenzymatic degradation by the host cell components and contamination by its proteins, expression characteristics such as the location of start and stop codons, and other factors recognized by those of skill in the art.

The recombinant nucleic acid molecule containing the MN gene, fragment thereof, or cDNA therefrom, may be employed to transform a host so as to permit that host (transformant) to express the structural gene or fragment thereof and to produce the protein or polypeptide for which the hybrid DNA encodes. The recombinant nucleic acid molecule may also be employed to transform a host so as to permit that host on replication to produce additional recombinant nucleic acid molecules as a source of MN nucleic acid and fragments thereof. The selection of an appropriate host for either of those uses is controlled by a number of factors recognized in the art. These include, for example, compatibility with the chosen vector, toxicity of the co-products, ease of recovery of the desired protein or polypeptide, expression characteristics, biosafety and costs.

Where the host cell is a procaryote such as E. coli, competent cells which are capable of DNA uptake are

prepared from cells harvested after exponential growth phase and subsequently treated by the $CaCl_2$ method by well known procedures. Transformation can also be performed after forming a protoplast of the host cell.

Where the host used is an eucaryote, transfection methods such as the use of a calcium phosphate-precipitate, electroporation, conventional mechanical procedures such as microinjection, insertion of a plasmid encapsulated in red blood cell ghosts or in liposomes, treatment of cells with agents such as lysophosphatidyl-choline or use of virus vectors, or the like may be used.

The level of production of a protein or polypeptide is governed by three major factors: (1) the number of copies of the gene or DNA sequence encoding for it within the cell; (2) the efficiency with which those gene and sequence copies are transcribed and translated; and (3) the stability of the mRNA. Efficiencies of transcription and translation (which together comprise expression) are in turn dependent upon nucleotide sequences, normally situated ahead of the desired coding sequence. Those nucleotide sequences or expression control sequences define, inter alia, the location at which an RNA polymerase interacts to initiate transcription (the promoter sequence) and at which ribosomes bind and interact with the mRNA (the product of transcription) to initiate translation. Not all such expression control sequences function with equal efficiency.

It is thus of advantage to separate the specific coding sequences for the desired protein from their adjacent nucleotide sequences and fuse them instead to known expression control sequences so as to favor higher levels of expression. This having been achieved, the newly engineered DNA fragment may be inserted into a multicopy plasmid or a bacteriophage derivative in order to increase the number of gene or sequence copies within the cell and thereby further improve the yield of expressed protein.

Several expression control sequences may be employed. These include the operator, promoter and ribosome binding and interaction sequences (including sequences such as the Shine-Dalgarno sequences) of the lactose operon of E. coli ("the lac system"), the corresponding sequences of the tryptophan synthetase system of E. coli ("the trp system"), a fusion of the trp and lac promoter ("the tac system"), the major operator and promoter regions of phage lambda (O_LP_L and O_RP_R,), and the control region of the phage fd coat protein. DNA fragments containing these sequences are excised by cleavage with restriction enzymes from the DNA isolated from transducing phages that carry the lac or trp operons, or from the DNA of phage lambda or fd. Those fragments are then manipulated in order to obtain a limited population of molecules such that the essential controlling sequences can be joined very close to, or in juxtaposition with, the initiation codon of the coding sequence.

The fusion product is then inserted into a cloning vehicle for transformation or transfection of the appropriate hosts and the level of antigen production is measured. Cells giving the most efficient expression may be thus selected. Alternatively, cloning vechicles carrying the lac, trp or lambda P_L control system attached to an initiation codon may be employed and fused to a fragment containing a sequence coding for a MN protein or polypeptide such that the gene or sequence is correctly translated from the initiation codon of the cloning vehicle.

The phrase "recombinant nucleic acid molecule" is herein defined to mean a hybrid nucleotide sequence comprising at least two nucleotide sequences, the first sequence not normally being found together in nature with the second.

The phrase "expression control sequence" is herein defined to mean a sequence of nucleotides that controls and regulates expression of structural genes when operatively linked to those genes.

The following are representative examples of genetically engineering MN proteins of this invention. The descriptions are exemplary and not meant to limit the invention in any way.

Production of Fusion Protein GEX-3X-MN

To confirm whether the partial cDNA clone codes for the p54/58N-specific protein, it was subcloned into the bacterial expression vector pGEX-3X [Pharmacia; Upsala, Sweden], constructed to express a fusion protein containing the C-terminus of glutathione S-transferase. The partial cDNA insert from the above-described pBluescript-MN was released by digesting the plasmid DNA by NotI. It was then treated with S1 nuclease to obtain blunt ends and then cloned into a dephosphorylated SmaI site of pGEX-3X [Pharmacia]. After transformation of XL1-Blue cells [E. coli strain; Stratagene] and induction with IPTG, a fusion protein was obtained.

The fusion protein--MN glutathione S-transferase (GEX-3X-MN) was purified by affinity chromatography on Glutathione-S-Sepharose 4B [Pharmacia]. Twenty micrograms of the purified recombinant protein in each of two parallel samples were separated by SDS-PAGE on a 10% gel. One of the samples (A) was stained with Coomassie brilliant blue, whereas the other (B) was blotted onto a Hybond C membrane [Amersham]. The blot was developed by autoradiography with ^{125}I-labeled MAb M75. The results are shown in Figure 2.

SDS-PAGE analysis provided an interesting result: a number of protein bands with different molecular weights (Figure 2A). A similar SDS-PAGE pattern was obtained with another representative fusion protein produced according to

this invention, beta-galactosidase-MN that was expressed from lambda gt11 lysogens.

By immunoblotting, a similar pattern was obtained: all the bands seen on stained SDS-PAGE gel reacted with the MN-specific MAb M75 (Figure 2B), indicating that all the protein bands are MN-specific. Also, that result indicates that the binding site for MAb M75 is on the N-terminal part of the MN protein, which is not affected by frameshifts.

As shown in Example 8 below, the fusion protein GEX-3X-MN was used in radioimmunoassays for MN-specific antibodies and for MN antigen.

Expression of MN 20-19 Protein

Another representative, recombinantly produced MN protein of this invention is the MN 20-19 protein which, when produced in baculovirus-infected Sf9 cells [Spodoptera frugiperda cells; Clontech; Palo Alto, CA (USA)], is glycosylated. The MN 20-19 protein misses the putative signal peptide (AAs 1-37) of SEQ. ID. NO.: 6 (Figure 1), has a methionine (Met) at the N-terminus for expression, and a Leu-Glu-His-His-His-His-His-His [SEQ. ID NO.: 22] added to the C-terminus for purification. In order to insert the portion of the MN coding sequence for the GEX-3X-MN fusion protein into alternate expression systems, a set of primers for PCR was designed. The primers were constructed to provide restriction sites at each end of the coding

sequence, as well as in-frame start and stop codons. The sequences of the primers, indicating restriction enzyme cleavage sites and expression landmarks, are shown below.

Primer #20:N-terminus

```
                          ┌Translation start
5'GTCGCTAGCTCCATGGGTCATATGCAGAGGTTGCCCCGGATGCAG 3'
     NheI  NcoI    NdeI  └MN cDNA #1      [SEQ. ID. NO. 17]
```

Primer #19:C-terminus

```
           ┌Translation stop
5'GAAGATCTCTTACTCGAGCATTCTCCAAGATCCAGCCTCTAGG 3'
   BglII     XhoI  └MN cDNA               [SEQ. ID. NO. 18]
```

The SEQ. ID. NOS.: 17 and 18 primers were used to amplify the MN coding sequence present in the pGEX-3X-MN vector using standard PCR techniques. The resulting PCR product (termed MN 20-19) was electrophoresed on a 0.5% agarose/1X TBE gel; the 1.3 kb band was excised; and the DNA recovered using the Gene Clean II kit according to the manufacturer's instructions [Bio101; LaJolla, CA (USA)].

MN 20-19 and plasmid pET-22b [Novagen, Inc.; Madison, WI (USA)] were cleaved with the restriction enzymes NdeI and XhoI, phenol-chloroform extracted, and the appropriate bands recovered by agarose gel electrophoresis as above. The isolated fragments were ethanol co-

precipitated at a vector:insert ratio of 1:4. After resuspension, the fragments were ligated using T4 DNA ligase. The resulting product was used to transform competent Novablue E. coli cells [Novagen, Inc.]. Plasmid mini-preps [Magic Minipreps; Promega] from the resultant ampicillin resistant colonies were screened for the presence of the correct insert by restriction mapping. Insertion of the gene fragment into the pET-22b plasmid using the NdeI and XhoI sites added a 6-histidine tail to the protein that could be used for affinity isolation.

To prepare MN 20-19 for insertion into the baculovirus expression system, the MN 20-19 gene fragment was excised from pET-22b using the restriction endonucleases XbaI and PvuI. The baculovirus shuttle vector pBacPAK8 [Clontech] was cleaved with XbaI and PacI. The desired fragments (1.3 kb for MN 20-19 and 5.5 kb for pBacPAK8) were isolated by agarose gel electrophoresis, recovered using Gene Clean II, and co-precipitated at an insert:vector ratio of 2.4:1.

After ligation with T4 DNA ligase, the DNA was used to transform competent NM522 E. coli cells (Stratagene). Plasmid mini-preps from resultant ampicillin resistant colonies were screened for the presence of the correct insert by restriction mapping. Plasmid DNA from an appropriate colony and linearized BacPAK6 baculovirus DNA [Clontech] were used to transform Sf9 cells by standard

techniques. Recombination produced BacPAK viruses carrying the MN 20-19 sequence. Those viruses were plated onto Sf9 cells and overlaid with agar.

Plaques were picked and plated onto Sf9 cells. The conditioned media and cells were collected. A small aliquot of the conditioned media was set aside for testing. The cells were extracted with PBS with 1% Triton X100.

The conditioned media and the cell extracts were dot blotted onto nitrocellulose paper. The blot was blocked with 5% non-fat dried milk in PBS. Mab M75 were used to detect the MN 20-19 protein in the dot blots. A rabbit anti-mouse Ig-HRP was used to detect bound Mab M75. The blots were developed with TMB/H_2O_2 with a membrane enhancer [KPL; Gaithersburg, MD (USA)]. Two clones producing the strongest reaction on the dot blots were selected for expansion. One was used to produce MN 20-19 protein in High Five cells [Invitrogen Corp., San Diego, CA (USA); BTI-TN-5BI-4; derived from Trichoplusia ni egg cell homogenate]. MN 20-19 protein was purified from the conditioned media from the virus infected High Five cells.

The MN 20-19 protein was purified from the conditioned media by immunoaffinity chromatography. 6.5 mg of Mab M75 was coupled to 1 g of Tresyl activated Toyopearl™ [Tosoh, Japan (#14471)]. Approximately 150 ml of the conditioned media was run through the M75-Toyopearl column. The column was washed with PBS, and the MN 20-19

protein was eluted with 1.5 M MgCl. The eluted protein was then dialyzed against PBS.

Fusion Proteins with C-Terminal Part Including Transmembrane Region Replaced by Fc or PA

MN fusion proteins in which the C terminal part including the transmembrane region is replaced by the Fc fragment of human IgG or by Protein A were constructed. Such fusion proteins are useful to identify MN binding protein(s). In such MN chimaeras, the whole N-terminal part of MN is accessible to interaction with heterologous proteins, and the C terminal tag serves for simple detection and purification of protein complexes.

Fusion Protein MN-PA (Protein A)

In a first step, the 3' end of the MN cDNA encoding the transmembrane region of the MN protein was deleted. The plasmid pFLMN (e.g. pBluescript with full length MN cDNA) was cleaved by *Eco*RI and blunt ended by S1 nuclease. Subsequent cleavage by *Sac*I resulted in the removal of the *Eco*RI-*Sac*I fragment. The deleted fragment was then replaced by a Protein A coding sequence that was derived from plasmid pEZZ (purchased from Pharmacia), which had been cleaved with *Rsa*I and *Sac*I. The obtained MN-PA construct was subcloned into a eukaryotic expression vector

pSG5C (described in Example 15), and was then ready for transfection experiments.

Fusion Protein MN-Fc

The cloning of the fusion protein MN-Fc was rather complicated due to the use of a genomic clone containing the Fc fragment of human IgG which had a complex structure in that it contained an enhancer, a promoter, exons and introns. Moreover, the complete sequence of the clone was not available. Thus, it was necessary to ensure the correct in-phase splicing and fusion of MN to the Fc fragment by the addition of a synthetic splice donor site (SSDS) designed according to the splicing sequences of the MN gene.

The construction procedure was as follows:

1. Plasmid pMH4 (e.g. pSV2*gpt* containing a genomic clone of the human IgG Fc region) was cleaved by *BamHI* in order to get a 13 kb fragment encoding Fc. [In pSV2*gpt*, the E. coli xanthine-guanine phosphoribosyl transferase gene (*gpt*) is expressed using the SV40 early promoter (P_E) located in the SV40 origin, the SV40 small T intron, and the SV40 polyadenylation site.]

2. At the same time, plasmid pFLMN (with full length MN cDNA) was cleaved by *SalI-EcoRI*. The released fragment was purified and ligated with a synthetic adapter *EcoRI-BglII* containing a synthetic splice donor site (SSDS).

3. Simultaneously, the plasmid pBKCMV was cleaved by *SalI-BamHI*. Then advantage was taken of the fact that the *BamHI* cohesive ends (of the Fc coding fragment) are compatible with the *BglII* ends of the SSDS, and Fc was ligated to MN. The MN-Fc ligation product was then inserted into pBKCMV by directional cloning through the *SalI* and *BamHI* sites.

Verification of the correct orientation and in-phase fusion of the obtained MN-Fc chimaeric clones was problematic in that the sequence of Fc was not known. Thus, functional constructs are selected on the basis of results of transient eukaryotic expression analyses.

Synthetic and Biologic Production of MN Proteins and Polypeptides

MN proteins and polypeptides of this invention may be prepared not only by recombinant means but also by synthetic and by other biologic means. Synthetic formation of the polypeptide or protein requires chemically synthesizing the desired chain of amino acids by methods well known in the art. Exemplary of other biologic means to prepare the desired polypeptide or protein is to subject to selective proteolysis a longer MN polypeptide or protein containing the desired amino acid sequence; for example, the longer polypeptide or protein can be split with chemical reagents or with enzymes.

Chemical synthesis of a peptide is conventional in the art and can be accomplished, for example, by the Merrifield solid phase synthesis technique [Merrifield, J., Am. Chem. Soc., 85: 2149-2154 (1963); Kent et al., Synthetic Peptides in Biology and Medicine, 29 f.f. eds. Alitalo et al., (Elsevier Science Publishers 1985); and Haug, J.D., "Peptide Synthesis and Protecting Group Strategy", American Biotechnology Laboratory, 5(1): 40-47 (Jan/Feb. 1987)].

Techniques of chemical peptide synthesis include using automatic peptide synthesizers employing commercially available protected amino acids, for example, Biosearch [San Rafael, CA (USA)] Models 9500 and 9600; Applied Biosystems, Inc. [Foster City, CA (USA)] Model 430; Milligen [a division of Millipore Corp.; Bedford, MA (USA)] Model 9050; and Du Pont's RAMP (Rapid Automated Multiple Peptide Synthesis) [Du Pont Compass, Wilmington, DE (USA)].

Regulation of MN Expression and MN Promoter

MN appears to be a novel regulatory protein that is directly involved in the control of cell proliferation and in cellular transformation. In HeLa cells, the expression of MN is positively regulated by cell density. Its level is increased by persistent infection with LCMV. In hybrid cells between HeLa and normal fibroblasts, MN expression correlates with tumorigenicity. The fact that MN

is not present in nontumorigenic hybrid cells (CGL1), but is expressed in a tumorigenic segregant lacking chromosome 11, indicates that MN is negatively regulated by a putative suppressor in chromosome 11.

Evidence supporting the regulatory role of MN protein was found in the generation of stable transfectants of NIH 3T3 cells that constitutively express MN protein as described in Example 15. As a consequence of MN expression, the NIH 3T3 cells acquired features associated with a transformed phenotype: altered morphology, increased saturation density, proliferative advantage in serum-reduced media, enhanced DNA synthesis and capacity for anchorage-independent growth. Further, as shown in Example 16, flow cytometric analyses of asynchronous cell populations indicated that the expression of MN protein leads to accelerated progression of cells through G1 phase, reduction of cell size and the loss of capacity for growth arrest under inappropriate conditions. Also, Example 16 shows that MN expressing cells display a decreased sensitivity to the DNA damaging drug mitomycin C.

Nontumorigenic human cells, CGL1 cells, were also transfected with the full-length MN cDNA. The same pSG5C-MN construct in combination with pSV2neo plasmid as used to transfect the NIH 3T3 cells (Example 15) was used. Also the protocol was the same except that the G418 concentration was increased to 1000 μg/ml.

Out of 15 MN-positive clones (tested by SP-RIA and Western blotting), 3 were chosen for further analysis. Two MN-negative clones isolated from CGL1 cells transfected with empty plasmid were added as controls. Initial analysis indicates that the morphology and growth habits of MN-transfected CGL1 cells are not changed dramatically, but their proliferation rate and plating efficiency is increased.

MN cDNA and promoter. When the promoter region from the MN genomic clone, isolated as described above, was linked to MN cDNA and transfected into CGL1 hybrid cells, expression of MN protein was detectable immediately after selection. However, then it gradually ceased, indicating thus an action of a feedback regulator. The putative regulatory element appeared to be acting via the MN promoter, because when the full-length cDNA (not containing the promoter) was used for transfection, no similar effect was observed.

An "antisense" MN cDNA/MN promoter construct was used to transfect CGL3 cells. The effect was the opposite of that of the CGL1 cells transfected with the "sense" construct. Whereas the transfected CGL1 cells formed colonies several times larger than the control CGL1, the transfected CGL3 cells formed colonies much smaller than the control CGL3 cells.

For those experiments, the part of the promoter region that was linked to the MN cDNA through a BamHI site was derived from a NcoI - BamHI fragment of the MN genomic clone [Bd3] and represents a region a few-hundred bp upstream from the transcription initiation site. After the ligation, the joint DNA was inserted into a pBK-CMV expression vector [Stratagene]. The required orientation of the inserted sequence was ensured by directional cloning and subsequently verified by restriction analysis. The tranfection procedure was the same as used in transfecting the NIH 3T3 cells (Example 15), but co-transfection with the pSV2neo plasmid was not necessary since the neo selection marker was already included in the pBK-CMV vector.

After two weeks of selection in a medium containing G418, remarkable differences between the numbers and sizes of the colonies grown were evident as noted above. Immediately following the selection and cloning, the MN-transfected CGL1 and CGL3 cells were tested by SP-RIA for expression and repression of MN, respectively. The isolated transfected CGL1 clones were MN positive (although the level was lower than obtained with the full-length cDNA), whereas MN protein was almost absent from the transfected CGL3 clones. However, in subsequent passages, the expression of MN in transfected CGL1 cells started to cease, and was then blocked perhaps evidencing a control feedback mechanism.

As a result of the very much lowered proliferation of the transfected CGL3 cells, it was difficult to expand the majority of cloned cells (according to SP-RIA, those with the lowest levels of MN), and they were lost during passaging. However, some clones overcame that problem and again expressed MN. It is possible that once those cells reached a higher quantity, that the level of endogenously produced MN mRNA increased over the amount of ectopically expressed antisense mRNA.

Transformation and Reversion

As illustrated in Examples 15 and 16, vertebrate cells transfected with MN cDNA in suitable vectors show striking morphologic transformation. Transformed cells may be very small, densely packed, slowly growing, with basophilic cytoplasm and enlarged Golgi apparatus. However, it has been found that transformed clones revert over time, for example, within 3-4 weeks, to nearly normal morphology, even though the cells may be producing MN protein at high levels. MN protein is biologically active even in yeast cells; depending upon the level of its expression, it stimulates or retards their growth and induces morphologic alterations.

Full-length MN cDNA was inserted into pGD, a MLV-derived vector, which together with standard competent MLV (murine leukemia virus), forms an infectious, transmissible

complex [pGD-MN + MLV]. That complex also transforms vertebrate cells, such as, NIH 3T3 cells and mouse embryo fibroblasts BALB/c, which also revert to nearly normal morphology. Such revertants again contain MN protein and produce the [pGD-MN + MLV] artificial virus complex, which retains its transforming capacity. Thus, reversion of MN-transformed cells is apparently not due to a loss, silencing or mutation of MN cDNA, but may be the result of the activation of suppressor gene(s).

Nucleic Acid Probes and Test Kits

Nucleic acid probes of this invention are those comprising sequences that are complementary or substantially complementary to the MN cDNA sequence shown in Figure 1 or to other MN gene sequences, such as, the complete genomic sequence of Figure 15 a-d [SEQ. ID. NO.: 5] and the putative promoter sequence [SEQ. ID. NO.: 27 of Figure 25]. The phrase "substantially complementary" is defined herein to have the meaning as it is well understood in the art and, thus, used in the context of standard hybridization conditions. The stringency of hybridization conditions can be adjusted to control the precision of complementarity. Exemplary are the stringent hybridization conditions used in Examples 11 and 12. Two nucleic acids are, for example, substantially complementary to each other, if they hybridize to each other under such stringent hybridization conditions.

Stringent hybridization conditions are considered herein to conform to standard hybridization conditions understood in the art to be stringent. For example, it is generally understood that stringent conditions encompass relatively low salt and/or high temperature conditions, such as provided by 0.02 M to 0.15 M NaCl at temperatures of 50°C to 70°C. Less stringent conditions, such as, 0.15 M to 0.9 M salt at temperatures ranging from 20°C to 55°C can be made more stringent by adding increasing amounts of formamide, which serves to destabilize hybrid duplexes as does increased temperature.

Exemplary stringent hybridization conditions are described in Examples 11 and 12, infra; the hybridizations therein were carried out "in the presence of 50% formamide at 42°C." [See Sambrook et al., Molecular Cloning: A Laboratory Manual, pages 1.91 and 9.47-9.51 (Second Edition, Cold Spring Harbor Laboratory Press; Cold Spring Harbor, NY; 1989); Maniatis et al., Molecular Cloning: A Laboratory Manual, pages 387-389 (Cold Spring Harbor Laboratory; Cold Spring Harbor, NY; 1982); Tsuchiya et al., Oral Surgery, Oral Medicine, Oral Pathology, 71(6): 721-725 (June 1991).]

Preferred nucleic acid probes of this invention are fragments of the isolated nucleic acid sequences that encode MN proteins or polypeptides according to this invention. Preferably those probes are composed of at least fifty nucleotides.

However, nucleic acid probes of this invention need not hybridize to a coding region of MN. For example, nucleic acid probes of this invention may hybridize partially or wholly to a non-coding region of the genomic sequence shown in Figure 15a-d [SEQ. ID. NO.: 5]. Conventional technology can be used to determine whether fragments of SEQ. ID. NO.: 5 or related nucleic acids are useful to identify MN nucleic acid sequences. [See, for example, Benton and Davis, supra and Fuscoe et al., supra.]

Areas of homology of the MN nt sequence to other non-MN nt sequences are indicated above. In general, nucleotide sequences that are not in the Alu or LTR-like regions of preferably 29 bases or more, or still more preferably of 50 bases or more, can be routinely tested and screened and found to hybridize under stringent conditions to only MN nucleotide sequences. Further, not all homologies within the Alu-like MN genomic sequences are so close to Alu repeats as to give a hybridization signal under stringent hybridization conditions. The percent of homology between MN Alu-like regions and a standard Alu-J sequence are indicated as follows:

Region of Homology within MN Genomic Sequence [SEQ. ID. NO.: 5; Figure 15a-d]	SEQ. ID. NOS.	% Homology to Entire Alu-J Sequence
921-1212	59	89.1%
2370-2631	60	78.6%
4587-4880	61	90.1%
6463-6738	62	85.4%
7651-7939	63	91.0%
9020-9317	64	69.8%

		% Homology to One Half of Alu-J Sequence
8301-8405	65	88.8%
10040-10122	66	73.2%.

Nucleic acid probes of this invention can be used to detect MN DNA and/or RNA, and thus can be used to test for the presence or absence of MN genes, and amplification(s), mutation(s) or genetic rearrangements of MN genes in the cells of a patient. For example, overexpression of an MN gene may be detected by Northern blotting and RNase protection analysis using probes of this invention. Gene alterations, as amplifications, translocations, inversions, and deletions among others, can be detected by using probes of this invention for *in situ* hybridization to chromosomes from a patient's cells, whether in metaphase spreads or interphase nuclei. Southern blotting could also be used with the probes of this

invention to detect amplifications or deletions of MN genes. Restriction Fragment Length Polymorphism (RFLP) analysis using said probes is a preferred method of detecting gene alterations, mutations and deletions. Said probes can also be used to identify MN proteins and/or polypeptides as well as homologs or near homologs thereto by their hybridization to various mRNAs transcribed from MN genes in different tissues.

Probes of this invention thus can be useful diagnostically/ prognostically. Said probes can be embodied in test kits, preferably with appropriate means to enable said probes when hybridized to an appropriate MN gene or MN mRNA target to be visualized. Such samples include tissue specimens including smears, body fluids and tissue and cell extracts.

PCR Assays. To detect relatively large genetic rearrangements, hybridization tests can be used. To detect relatively small genetic rearrangements, as, for example, small deletions or amplifications, or point mutations, the polymerase chain reaction (PCR) would preferably be used. [U.S. Patent Nos. 4,800,159; 4,683,195; 4,683,202; and Chapter 14 of Sambrook et al., Molecular Cloning: A Laboratory Manual, supra]

An exemplary assay would use cellular DNA from normal and cancerous cells, which DNA would be isolated and amplified employing appropriate PCR primers. The PCR

products would be compared, preferably initially, on a sizing gel to detect size changes indicative of certain genetic rearrangements. If no differences in sizes are noted, further comparisons can be made, preferably using, for example, PCR-single-strand conformation polymorphism (PCR-SSCP) assay or a denaturing gradient gel electrophoretic assay. [See, for example, Hayashi, K., "PCR-SSCP: A Simple and Sensitive Method for Detection of Mutations in the Genomic DNA," in PCR Methods and Applications, 1: 34-38 (1991); and Meyers et al., "Detection and Localization of Single Base Changes by Denaturing Gradient Gel Electrophoresis," Methods in Enzymology, 155: 501 (1987).]

Assays

Assays according to this invention are provided to detect and/or quantitate MN antigen or MN-specific antibodies in vertebrate samples, preferably mammalian samples, more preferably human samples. Such samples include tissue specimens, body fluids, tissue extracts and cell extracts. MN antigen may be detected by immunoassay, immunohistochemical staining, immunoelectron and scanning microscopy using immunogold among other techniques.

Preferred tissue specimens to assay by immunohistochemical staining include cell smears, histological sections from biopsied tissues or organs, and

imprint preparations among other tissue samples. Such tissue specimens can be variously maintained, for example, they can be fresh, frozen, or formalin-, alcohol- or acetone- or otherwise fixed and/or paraffin-embedded and deparaffinized. Biopsied tissue samples can be, for example, those samples removed by aspiration, bite, brush, cone, chorionic villus, endoscopic, excisional, incisional, needle, percutaneous punch, and surface biopsies, among other biopsy techniques.

Preferred cervical tissue specimens include cervical smears, conization specimens, histologic sections from hysterectomy specimens or other biopsied cervical tissue samples. Preferred means of obtaining cervical smears include routine swab, scraping or cytobrush techniques, among other means. More preferred are cytobrush or swab techniques. Preferably, cell smears are made on microscope slides, fixed, for example, with 55% EtOH or an alcohol based spray fixative and air-dried.

Papanicolaou-stained cervical smears (Pap smears) can be screened by the methods of this invention, for example, for retrospective studies. Preferably, Pap smears would be decolorized and re-stained with labeled antibodies against MN antigen. Also archival specimens, for example, matched smears and biopsy and/or tumor specimens, can be used for retrospective studies. Prospective studies can also be done with matched specimens from patients that have

a higher than normal risk of exhibiting abnormal cervical cytopathology.

Preferred samples in which to assay MN antigen by, for example, Western blotting or radioimmunoassay, are tissue and/or cell extracts. However, MN antigen may be detected in body fluids, which can include among other fluids: blood, serum, plasma, semen, breast exudate, saliva, tears, sputum, mucous, urine, lymph, cytosols, ascites, pleural effusions, amniotic fluid, bladder washes, bronchioalveolar lavages and cerebrospinal fluid. It is preferred that the MN antigen be concentrated from a larger volume of body fluid before testing. Preferred body fluids to assay would depend on the type of cancer for which one was testing, but in general preferred body fluids would be breast exudate, pleural effusions and ascites.

MN-specific antibodies can be bound by serologically active MN proteins/polypeptides in samples of such body fluids as blood, plasma, serum, lymph, mucous, tears, urine, spinal fluid and saliva; however, such antibodies are found most usually in blood, plasma and serum, preferably in serum. A representative assay to detect MN-specific antibodies is shown in Example 8 below wherein the fusion protein GEX-3X-MN is used. Correlation of the results from the assays to detect and/or quantitate MN antigen and MN-specific antibodies reactive therewith,

provides a preferred profile of the disease condition of a patient.

The assays of this invention are both diagnostic and/or prognostic, i.e., diagnostic/prognostic. The term "diagnostic/ prognostic" is herein defined to encompass the following processes either individually or cumulatively depending upon the clinical context: determining the presence of disease, determining the nature of a disease, distinguishing one disease from another, forecasting as to the probable outcome of a disease state, determining the prospect as to recovery from a disease as indicated by the nature and symptoms of a case, monitoring the disease status of a patient, monitoring a patient for recurrence of disease, and/or determining the preferred therapeutic regimen for a patient. The diagnostic/prognostic methods of this invention are useful, for example, for screening populations for the presence of neoplastic or pre-neoplastic disease, determining the risk of developing neoplastic disease, diagnosing the presence of neoplastic and/or pre-neoplastic disease, monitoring the disease status of patients with neoplastic disease, and/or determining the prognosis for the course of neoplastic disease. For example, it appears that the intensity of the immunostaining with MN-specific antibodies may correlate with the severity of dysplasia present in samples tested.

The present invention is useful for screening for the presence of a wide variety of neoplastic diseases including carcinomas, such as, mammary, urinary tract, ovarian, uterine, cervical, endometrial, squamous cell and adenosquamous carcinomas; head and neck cancers; mesodermal tumors, such as, neuroblastomas and retinoblastomas; sarcomas, such as osteosarcomas and Ewing's sarcoma; and melanomas. Of particular interest are gynecological cancers including ovarian, uterine, cervical, vaginal, vulval and endometrial cancers, particularly ovarian, uterine cervical and endometrial cancers. Also of particular interest are cancers of the breast, of the stomach including esophagus, of the colon, of the kidney, of the prostate, of the liver, of the urinary tract including bladder, of the lung, and of the head and neck.

The invention provides methods and compositions for evaluating the probability of the presence of malignant or pre-malignant cells, for example, in a group of cells freshly removed from a host. Such an assay can be used to detect tumors, quantitate their growth, and help in the diagnosis and prognosis of disease. The assays can also be used to detect the presence of cancer metastasis, as well as confirm the absence or removal of all tumor tissue following surgery, cancer chemotherapy and/or radiation therapy. It can further be used to monitor cancer chemotherapy and tumor reappearance.

The presence of MN antigen or antibodies can be detected and/or quantitated using a number of well-defined diagnostic assays. Those in the art can adapt any of the conventional immunoassay formats to detect and/or quantitate MN antigen and/or antibodies. Example 8 details the format of a preferred diagnostic method of this invention--a radioimmunoassay. Immunohistochemical staining is another preferred assay format as exemplified in Example 13.

Many other formats for detection of MN antigen and MN-specific antibodies are, of course available. Those can be Western blots, ELISAs (enzyme-linked immunosorbent assays), RIAs (radioimmunoassay), competitive EIA or dual antibody sandwich assays, among other assays all commonly used in the diagnostic industry. In such immunoassays, the interpretation of the results is based on the assumption that the antibody or antibody combination will not cross-react with other proteins and protein fragments present in the sample that are unrelated to MN.

Representative of one type of ELISA test for MN antigen is a format wherein a microtiter plate is coated with antibodies made to MN proteins/polypeptides or antibodies made to whole cells expressing MN proteins, and to this is added a patient sample, for example, a tissue or cell extract. After a period of incubation permitting any antigen to bind to the antibodies, the plate is washed and another set of anti-MN antibodies which are linked to an

enzyme is added, incubated to allow reaction to take place, and the plate is then rewashed. Thereafter, enzyme substrate is added to the microtiter plate and incubated for a period of time to allow the enzyme to work on the substrate, and the adsorbance of the final preparation is measured. A large change in absorbance indicates a positive result.

It is also apparent to one skilled in the art of immunoassays that MN proteins and/or polypeptides can be used to detect and/or quantitate the presence of MN antigen in the body fluids, tissues and/or cells of patients. In one such embodiment, a competition immunoassay is used, wherein the MN protein/polypeptide is labeled and a body fluid is added to compete the binding of the labeled MN protein/polypeptide to antibodies specific to MN protein/polypeptide. Such an assay can be used to detect and/or quantitate MN antigen as described in Example 8.

In another embodiment, an immunometric assay may be used wherein a labeled antibody made to a MN protein or polypeptide is used. In such an assay, the amount of labeled antibody which complexes with the antigen-bound antibody is directly proportional to the amount of MN antigen in the sample.

A representative assay to detect MN-specific antibodies is a competition assay in which labeled MN protein/polypeptide is precipitated by antibodies in a

sample, for example, in combination with monoclonal antibodies recognizing MN proteins/polypeptides. One skilled in the art could adapt any of the conventional immunoassay formats to detect and/or quantitate MN-specific antibodies. Detection of the binding of said antibodies to said MN protein/polypeptide could be by many ways known to those in the art, e.g., in humans with the use of anti-human labeled IgG.

An exemplary immunoassay method of this invention to detect and/or quantitate MN antigen in a vertebrate sample comprises the steps of:

a) incubating said vertebrate sample with one or more sets of antibodies (an antibody or antibodies) that bind to MN antigen wherein one set is labeled or otherwise detectable;

b) examining the incubated sample for the presence of immune complexes comprising MN antigen and said antibodies.

Another exemplary immunoassay method according to this invention is that wherein a competition immunoassay is used to detect and/or quantitate MN antigen in a vertebrate sample and wherein said method comprises the steps of:

a) incubating a vertebrate sample with one or more sets of MN-specific antibodies and a certain amount of a labeled or otherwise detectable MN protein/polypeptide

wherein said MN protein/ polypeptide competes for binding to said antibodies with MN antigen present in the sample;

b) examining the incubated sample to determine the amount of labeled/detectable MN protein/polypeptide bound to said antibodies; and

c) determining from the results of the examination in step b) whether MN antigen is present in said sample and/or the amount of MN antigen present in said sample.

Once antibodies (including biologically active antibody fragments) having suitable specificity have been prepared, a wide variety of immunological assay methods are available for determining the formation of specific antibody-antigen complexes. Numerous competitive and non-competitive protein binding assays have been described in the scientific and patent literature, and a large number of such assays are commercially available. Exemplary immunoassays which are suitable for detecting a serum antigen include those described in U.S. Patent Nos. 3,791,932; 3,817,837; 3,839,153; 3,850,752; 3,850,578; 3,853,987; 3,867,517; 3,879,262; 3,901,654; 3,935,074; 3,984,533; 3,996,345; 4,034,074; and 4,098,876.

Antibodies employed in assays may be labeled or unlabeled. Unlabeled antibodies may be employed in agglutination; labeled antibodies may be employed in a wide variety of assays, employing a wide variety of labels.

Suitable detection means include the use of labels such as radionuclides, enzymes, coenzymes, fluorescers, chemiluminescers, chromogens, enzyme substrates or co-factors, enzyme inhibitors, free radicals, particles, dyes and the like. Such labeled reagents may be used in a variety of well known assays, such as radioimmunoassays, enzyme immunoassays, e.g., ELISA, fluorescent immunoassays, and the like. See for example, U.S. Patent Nos. 3,766,162; 3,791,932; 3,817,837; and 4,233,402.

Methods to prepare antibodies useful in the assays of the invention are described below. The examples below detail representative assays according to this invention.

Immunoassay Test Kits

The above outlined assays can be embodied in test kits to detect and/or quantitate MN antigen and/or MN-specific antibodies (including biologically active antibody fragments). Kits to detect and/or quantitate MN antigen can comprise MN protein(s)/polypeptides(s) and/or MN-specific antibodies, polyclonal and/or monoclonal. Such diagnostic/prognostic test kits can comprise one or more sets of antibodies, polyclonal and/or monoclonal, for a sandwich format wherein antibodies recognize epitopes on the MN antigen, and one set is appropriately labeled or is otherwise detectable.

Test kits for an assay format wherein there is competition between a labeled (or otherwise detectable) MN protein/polypeptide and MN antigen in the sample, for binding to an antibody, can comprise the combination of the labeled protein/polypeptide and the antibody in amounts which provide for optimum sensitivity and accuracy.

Test kits for MN-specific antibodies preferably comprise labeled/detectable MN proteins(s) and/or polypeptides(s), and may comprise other components as necessary, for example, to perform a preferred assay as outlined in Example 8 below, such as, controls, buffers, diluents and detergents. Such test kits can have other appropriate formats for conventional assays.

A kit for use in an enzyme-immunoassay typically includes an enzyme-labelled reagent and a substrate for the enzyme. The enzyme can, for example, bind either an MN-specific antibody of this invention or to an antibody to such an MN-specific antibody.

Preparation of MN-Specific Antibodies

The term "antibodies" is defined herein to include not only whole antibodies but also biologically active fragments of antibodies, preferably fragments containing the antigen binding regions. Such antibodies may be prepared by conventional methodology and/or by genetic engineering. Antibody fragments may be genetically engineered, preferably

from the variable regions of the light and/or heavy chains (V_H and V_L), including the hypervariable regions, and still more preferably from both the V_H and V_L regions. For example, the term "antibodies" as used herein comprehends polyclonal and monoclonal antibodies and biologically active fragments thereof including among other possibilities "univalent" antibodies [Glennie et al., Nature, 295: 712 (1982)]; Fab proteins including Fab' and $F(ab')_2$ fragments whether covalently or non-covalently aggregated; light or heavy chains alone, preferably variable heavy and light chain regions (V_H and V_L regions), and more preferably including the hypervariable regions [otherwise known as the complementarity determining regions (CDRs) of said V_H and V_L regions]; F_c proteins; "hybrid" antibodies capable of binding more than one antigen; constant-variable region chimeras; "composite" immunoglobulins with heavy and light chains of different origins; "altered" antibodies with improved specificity and other characteristics as prepared by standard recombinant techniques and also by oligonucleotide-directed mutagenesis techniques [Dalbadie-McFarland et al., PNAS (USA), 79: 6409 (1982)].

It may be preferred for therapeutic and/or imaging uses that the antibodies be biologically active antibody fragments, preferably genetically engineered fragments, more preferably genetically engineered fragments from the V_H

and/or V_L regions, and still more preferably comprising the hypervariable regions thereof.

There are conventional techniques for making polyclonal and monoclonal antibodies well-known in the immunoassay art. Immunogens to prepare MN-specific antibodies include MN proteins and/or polypeptides, preferably purified, and MX-infected tumor line cells, for example, MX-infected HeLa cells, among other immunogens.

Anti-peptide antibodies are also made by conventional methods in the art as described in European Patent Publication No. 44,710 (published Jan. 27, 1982). Briefly, such anti-peptide antibodies are prepared by selecting a peptide from an MN amino acid sequence as from Figure 1, chemically synthesizing it, conjugating it to an appropriate immunogenic protein and injecting it into an appropriate animal, usually a rabbit or a mouse; then, either polyclonal or monoclonal antibodies are made, the latter by a Kohler-Milstein procedure, for example.

Besides conventional hybridoma technology, newer technologies can be used to produce antibodies according to this invention. For example, the use of the PCR to clone and express antibody V-genes and phage display technology to select antibody genes encoding fragments with binding activities has resulted in the isolation of antibody fragments from repertoires of PCR amplified V-genes using immunized mice or humans. [Marks et al., BioTechnology, 10:

779 (July 1992) for references; Chiang et al., BioTechniques, 7(4): 360 (1989); Ward et al., Nature, 341: 544 (Oct. 12, 1989); Marks et al., J. Mol. Biol., 222: 581 (1991); Clackson et al., Nature, 352: (15 August 1991); and Mullinax et al., PNAS (USA), 87: 8095 (Oct. 1990).]

Descriptions of preparing antibodies, which term is herein defined to include biologically active antibody fragments, by recombinant techniques can be found in U.S. Patent No. 4,816,567 (issued March 28, 1989); European Patent Application Publication Number (EP) 338,745 (published Oct. 25, 1989); EP 368,684 (published June 16, 1990); EP 239,400 (published September 30, 1987); WO 90/14424 (published Nov. 29, 1990); WO 90/14430 (published May 16, 1990); Huse et al., Science, 246: 1275 (Dec. 8, 1989); Marks et al., BioTechnology, 10: 779 (July 1992); La Sastry et al., PNAS (USA), 86: 5728 (August 1989); Chiang et al., BioTechniques, 7(40): 360 (1989); Orlandi et al., PNAS (USA), 86: 3833 (May 1989); Ward et al. Nature, 341: 544 (October 12, 1989); Marks et al., J. Mol. Biol., 222: 581 (1991); and Hoogenboom et al., Nucleic Acids Res., 19(15): 4133 (1991).

Representative Mabs

Monoclonal antibodies for use in the assays of this invention may be obtained by methods well known in the art for example, Galfre and Milstein, "Preparation of

Monoclonal Antibodies: Strategies and Procedures," in Methods in Enzymology: Immunochemical Techniques, 73: 1-46 [Langone and Vanatis (eds); Academic Press (1981)]; and in the classic reference, Milstein and Kohler, Nature, 256: 495-497 (1975).]

Although representative hybridomas of this invention are formed by the fusion of murine cell lines, human/human hybridomas [Olsson et al., PNAS (USA), 77: 5429 (1980)] and human/murine hybridomas [Schlom et al., PNAS (USA), 77: 6841 (1980); Shearman et al. J. Immunol., 146: 928-935 (1991); and Gorman et al., PNAS (USA), 88: 4181-4185 (1991)] can also be prepared among other possiblities. Such humanized monoclonal antibodies would be preferred monoclonal antibodies for therapeutic and imaging uses.

Monoclonal antibodies specific for this invention can be prepared by immunizing appropriate mammals, preferably rodents, more preferably rabbits or mice, with an appropriate immunogen, for example, MaTu-infected HeLa cells, MN fusion proteins, or MN proteins/polypeptides attached to a carrier protein if necessary. Exemplary methods of producing antibodies of this invention are described below.

The monoclonal antibodies useful according to this invention to identify MN proteins/polypeptides can be labeled in any conventional manner, for example, with enzymes such as horseradish peroxidase (HRP), fluorescent

compounds, or with radioactive isotopes such as, ^{125}I, among other labels. A preferred label, according to this invention is ^{125}I, and a preferred method of labeling the antibodies is by using chloramine-T [Hunter, W.M., "Radioimmunoassay," In: Handbook of Experimental Immunology, pp. 14.1-14.40 (D.W. Weir ed.; Blackwell, Oxford/London/Edinburgh/Melbourne; 1978)].

Representative mabs of this invention include Mabs M75, MN9, MN12 and MN7 described below. Monoclonal antibodies of this invention serve to identify MN proteins/polypeptides in various laboratory diagnostic tests, for example, in tumor cell cultures or in clinical samples.

Mabs Prepared Against HeLa Cells

MAb M75. Monoclonal antibody M75 (MAb M75) is produced by mouse lymphocytic hybridoma VU-M75, which was initially deposited in the Collection of Hybridomas at the Institute of Virology, Slovak Academy of Sciences (Bratislava, Czechoslovakia) and was deposited under ATCC Designation HB 11128 on September 17, 1992 at the American Type Culture Collection (ATCC) in Rockville, MD (USA).

Hybridoma VU-M75 was produced according to the procedure described in Gerhard, W., "Fusion of cells in suspension and outgrowth of hybrids in conditioned medium," In: Monoclonal Antibodies. Hybridomas: A New Dimension in

Biological Analysis, page 370 [Kennet et al. (eds.); Plenum NY (USA)]. BALB/C mice were immunized with MaTu-infected HeLa cells, and their spleen cells were fused with myeloma cell line NS-0. Tissue culture media from the hybridomas were screened for monoclonal antibodies, using as antigen the p58 immunoprecipitated from cell extracts of MaTu-infected HeLa with rabbit anti-MaTu serum and protein A-Staphylococcus aureus cells (SAC) [Zavada and Zavadova, Arch. Virol., 118 189-197 (1991)], and eluted from SDS-PAGE gels. Monoclonal antibodies were purified from TC media by affinity chromatography on protein A-Sepharose [Harlow and Lane, "Antibodies: A Laboratory Manual," Cold Spring Harbor, Cold Spring Harbor, NY (USA); 1988].

Mab M75 recognizes both the nonglycosylated GEX-3X-MN fusion protein and native MN protein as expressed in CGL3 cells equally well. Mab M75 was shown by epitope mapping to be reactive with the epitope represented by the amino acid sequence from AA 62 to AA 67 [SEQ. ID. NO.: 10] of the MN protein shown in Figure 1.

Mabs M16 and M67. Also produced by the method described for producing MAb M75 (isotype IgG2B) were MAbs M16 (isotype IgG2A) and M67 (isotype IgG1). Mabs M16 and M67 recognize MX protein, as described in the examples below.

MAb H460. Monoclonal antibody H460 (MAb H460) was prepared in a manner similar to that for MAb M75 except that

the mice were immunized with HeLa cells uninfected with MaTu, and lymphocytes of the mice rather than spleen cells were fused with cells from myeloma cell line NS-0. MAb H460 reacts about equally with any human cells.

Mabs Prepared Against Fusion Protein GEX-3X-MN

Monoclonal antibodies of this invention were also prepared against the MN glutathione S-transferase fusion protein (GEX-3X-MN) purified by affinity chromatography as described above. BALB/C mice were immunized intraperitoneally according to standard procedures with the GEX-3X-MN fusion protein in Freund's adjuvant. Spleen cells of the mice were fused with SP/20 myeloma cells [Milstein and Kohler, supra].

Tissue culture media from the hybridomas were screened against CGL3 and CGL1 membrane extracts in an ELISA employing HRP labelled-rabbit anti-mouse. The membrane extracts were coated onto microtiter plates. Selected were antibodies reacted with the CGL3 membrane extract. Selected hybridomas were cloned twice by limiting dilution.

The mabs prepared by the just described method were characterized by Western blots of the GEX-3X-MN fusion protein, and with membrane extracts from the CGL1 and CGL3 cells. Representative of the mabs prepared are Mabs MN9, MN12 and MN7.

Mab MN9. Monoclonal antibody MN9 (Mab MN9) reacts to the same epitope as Mab M75, represented by the sequence from AA 62 to AA 67 [SEQ. ID. NO.: 10] of the Figure 1 MN protein. As Mab M75, Mab MN9 recognizes both the GEX-3X-MN fusion protein and native MN protein equally well.

Mabs corresponding to Mab MN9 can be prepared reproducibly by screening a series of mabs prepared against an MN protein/polypeptide, such as, the GEX-3X-MN fusion protein, against the peptide representing the epitope for Mabs M75 and MN9, that is, SEQ. ID. NO.: 10. Alternatively, the Novatope system [Novagen] or competition with the deposited Mab M75 could be used to select mabs comparable to Mabs M75 and MN9.

Mab MN12. Monoclonal antibody MN12 (Mab MN12) is produced by the mouse lymphocytic hybridoma MN 12.2.2 which was deposited under ATCC Designation HB 11647 on June 9, 1994 at the American Type Culture Collection (ATCC) at 12301 Parklawn Drive, Rockville, MD 20852 (USA). Antibodies corresponding to Mab MN12 can also be made, analogously to the method outlined above for Mab MN9, by screening a series of antibodies prepared against an MN protein/polypeptide, against the peptide representing the epitope for Mab MN12. That peptide is AA 55 - AA 60 of Figure 1 [SEQ. ID. NO.: 11]. The Novatope system could also be used to find antibodies specific for said epitope.

Mab MN7. Monoclonal antibody MN7 (Mab MN7) was selected from mabs prepared against nonglycosylated GEX-3X-MN as described above. It recognizes the epitope on MN represented by the amino acid sequence from AA 127 to AA 147 [SEQ. ID. NO.: 12] of the Figure 1 MN protein. Analogously to methods described above for Mabs MN9 and MN12, mabs corresponding to Mab MN7 can be prepared by selecting mabs prepared against an MN protein/polypeptide that are reactive with the peptide having SEQ. ID. NO.: 12, or by the stated alternative means.

Epitope Mapping

Epitope mapping was performed by the Novatope system, a kit for which is commercially available from Novagen, Inc. [See, for analogous example, Li et al., Nature, 363: 85-88 (6 May 1993).] In brief, the MN cDNA was cut into overlapping short fragments of approximately 60 base pairs. The fragments were expressed in E. coli, and the E. coli colonies were transferred onto nitrocellulose paper, lysed and probed with the mab of interest. The MN cDNA of clones reactive with the mab of interest was sequenced, and the epitopes of the mabs were deduced from the overlapping polypeptides found to be reactive with each mab.

Therapeutic Use of MN-Specific Antibodies

The MN-specific antibodies of this invention, monoclonal and/or polyclonal, preferably monoclonal, and as outlined above, may be used therapeutically in the treatment of neoplastic and/or pre-neoplastic disease, either alone or in combination with chemotherapeutic drugs or toxic agents, such as ricin A. Further preferred for therapeutic use would be biologically active antibody fragments as described herein. Also preferred MN-specific antibodies for such therapeutic uses would be humanized monoclonal antibodies.

The MN-specific antibodies can be administered in a therapeutically effective amount, preferably dispersed in a physiologically acceptable, nontoxic liquid vehicle.

Imaging Use of Antibodies

Further, the MN-specific antibodies of this invention when linked to an imaging agent, such as a radionuclide, can be used for imaging. Biologically active antibody fragments or humanized monoclonal antibodies, may be preferred for imaging use.

A patient's neoplastic tissue can be identified as, for example, sites of transformed stem cells, of tumors and locations of any metastases. Antibodies, appropriately labeled or linked to an imaging agent, can be injected in a physiologically acceptable carrier into a patient, and the binding of the antibodies can be detected by a method

appropriate to the label or imaging agent, for example, by scintigraphy.

Antisense MN Nucleic Acid Sequences

MN genes are herein considered putative oncogenes and the encoded proteins thereby are considered to be putative oncoproteins. Antisense nucleic acid sequences substantially complementary to mRNA transcribed from MN genes, as represented by the antisense oligodeoxynucleotides (ODNs) of Example 10, infra, can be used to reduce or prevent expression of the MN gene. [Zamecnick, P.C., "Introduction: Oligonucleotide Base Hybridization as a Modulator of Genetic Message Readout," pp. 1-6, Prospects for Antisense Nucleic Acid Therapy of Cancer and AIDS, (Wiley-Liss, Inc., New York, NY, USA; 1991); Wickstrom, E., "Antisense DNA Treatment of HL-60 Promyelocytic Leukemia Cells: Terminal Differentiation and Dependence on Target Sequence," pp. 7-24, id.; Leserman et al., "Targeting and Intracellular Delivery of Antisense Oligonucleotides Interfering with Oncogene Expression," pp. 25-34, id.; Yokoyama, K., "Transcriptional Regulation of c-myc Proto-oncogene by Antisense RNA," pp. 35-52, id.; van den Berg et al., "Antisense fos Oligodeoxyribonucleotides Suppress the Generation of Chromosomal Aberrations," pp. 63-70, id.; Mercola, D., "Antisense fos and fun RNA," pp. 83-114, id.; Inouye, Gene, 72: 25-34 (1988); Miller and Ts'o, Ann.

Reports Med. Chem., 23: 295-304 (1988); Stein and Cohen, Cancer Res., 48: 2659-2668 (1988); Stevenson and Inversen, J. Gen. Virol., 70: 2673-2682 (1989); Goodchild, "Inhibition of Gene Expression by Oligonucleotides," pp. 53-77, Oligodeoxynucleotides: Antisense Inhibitors of Gene Expression (Cohen, J.S., ed; CRC Press, Boca Raton, Florida, USA; 1989); Dervan et al., "Oligonucleotide Recognition of Double-helical DNA by Triple-helix Formation," pp. 197-210, id.; Neckers, L.M., "Antisense Oligodeoxynucleotides as a Tool for Studying Cell Regulation: Mechanisms of Uptake and Application to the Study of Oncogene Function," pp. 211-232, id.; Leitner et al., PNAS (USA), 87: 3430-3434 (1990); Bevilacqua et al., PNAS (USA), 85: 831-835 (1988); Loke et al. Curr. Top. Microbiol. Immunol., 141: 282-288 (1988); Sarin et al., PNAS (USA), 85: 7448-7451 (1988); Agrawal et al., "Antisense Oligonucleotides: A Possible Approach for Chemotherapy and AIDS," International Union of Biochemistry Conference on Nucleic Acid Therapeutics (Jan. 13-17, 1991; Clearwater Beach, Florida, USA); Armstrong, L., Ber. Week, pp. 88-89 (March 5, 1990); and Weintraub et al., Trends, 1: 22-25 (1985).] Such antisense nucleic acid sequences, preferably oligonucleotides, by hybridizing to the MN mRNA, particularly in the vicinity of the ribosome binding site and translation initiation point, inhibits translation of the mRNA. Thus, the use of such antisense nucleic acid sequences may be considered to be a form of cancer therapy.

Preferred antisense oligonucleotides according to this invention are gene-specific ODNs or oligonucleotides complementary to the 5′ end of MN mRNA. Particularly preferred are the 29-mer ODN1 and 19-mer ODN2 for which the sequences are provided in Example 10, infra. Those antisense ODNs are representative of the many antisense nucleic acid sequences that can function to inhibit MN gene expression. Ones of ordinary skill in the art could determine appropriate antisense nucleic acid sequences, preferably antisense oligonucleotides, from the nucleic acid sequences of Figures 1 and 15a-d.

Also, as described above, CGL3 cells transfected with an "antisense" MN cDNA/promoter construct formed colonies much smaller than control CGL3 cells.

Vaccines

It will be readily appreciated that MN proteins and polypeptides of this invention can be incorporated into vaccines capable of inducing protective immunity against neoplastic disease and a dampening effect upon tumorigenic activity. Efficacy of a representative MN fusion protein GEX-3X-MN as a vaccine in a rat model is shown in Example 14.

MN proteins and/or polypeptides may be synthesized or prepared recombinantly or otherwise biologically, to comprise one or more amino acid sequences corresponding to

one or more epitopes of the MN proteins either in monomeric or multimeric form. Those proteins and/or polypeptides may then be incorporated into vaccines capable of inducing protective immunity. Techniques for enhancing the antigenicity of such polypeptides include incorporation into a multimeric structure, binding to a highly immunogenic protein carrier, for example, keyhole limpet hemocyanin (KLH), or diptheria toxoid, and administration in combination with adjuvants or any other enhancers of immune response.

Preferred MN proteins/polypeptides to be used in a vaccine according to this invention would be genetically engineered MN proteins. Preferred recombinant MN protein are the GEX-3X-MN, MN 20-19, MN-Fc and MN-PA proteins.

Other exemplary vaccines include vaccinia-MN (live vaccinia virus with full-length MN cDNA), and baculovirus-MN (full length MN cDNA inserted into baculovirus vector, e.g. in suspension of infected insect cells). Different vaccines may be combined and vaccination periods can be prolonged.

A preferred exemplary use of such a vaccine of this invention would be its administration to patients whose MN-carrying primary cancer had been surgically removed. The vaccine may induce active immunity in the patients and prevent recidivism or metastasis.

It will further be appreciated that anti-idiotype antibodies to antibodies to MN proteins/polypeptides are also useful as vaccines and can be similarly formulated.

An amino acid sequence corresponding to an epitope of an MN protein/polypeptide either in monomeric or multimeric form may also be obtained by chemical synthetic means or by purification from biological sources including genetically modified microorganisms or their culture media. [See Lerner, "Synthetic Vaccines", Sci. Am. 248(2): 66-74 (1983).] The protein/polypeptide may be combined in an amino acid sequence with other proteins/polypeptides including fragments of other proteins, as for example, when synthesized as a fusion protein, or linked to other antigenic or non-antigeneic polypeptides of synthetic or biological origin. In some instances, it may be desirable to fuse a MN protein or polypeptide to an immunogenic and/or antigenic protein or polypeptide, for example, to stimulate efficacy of a MN-based vaccine.

The term "corresponding to an epitope of an MN protein/polypeptide" will be understood to include the practical possibility that, in some instances, amino acid sequence variations of a naturally occurring protein or polypeptide may be antigenic and confer protective immunity against neoplastic disease and/or anti-tumorigenic effects. Possible sequence variations include, without limitation, amino acid substitutions, extensions, deletions,

truncations, interpolations and combinations thereof. Such variations fall within the contemplated scope of the invention provided the protein or polypeptide containing them is immunogenic and antibodies elicited by such a polypeptide or protein cross-react with naturally occurring MN proteins and polypeptides to a sufficient extent to provide protective immunity and/or anti-tumorigenic activity when administered as a vaccine.

Such vaccine compositions will be combined with a physiologically acceptable medium, including immunologically acceptable diluents and carriers as well as commonly employed adjuvants such as Freund's Complete Adjuvant, saponin, alum, and the like. Administration would be in immunologically effective amounts of the MN proteins or polypeptides, preferably in quantities providing unit doses of from 0.01 to 10.0 micrograms of immunologically active MN protein and/or polypeptide per kilogram of the recipient's body weight. Total protective doses may range from 0.1 to about 100 micrograms of antigen.

Routes of administration, antigen dose, number and frequency of injections are all matters of optimization within the scope of the ordinary skill in the art.

The following examples are for purposes of illustration only and not meant to limit the invention in any way.

Materials and Methods

The following materials and methods were used in examples below.

MaTu-Infected and Uninfected HeLa Cells

MaTu agent [Zavada et al., Nature New Biol., 240: 124-125 (1972); Zavada et al., J. Gen. Virol, 24: 327-337 (1974)] was from original "MaTu" cells [Widmaier et al., Arch. Geschwulstforsch, 44: 1-10 (1974)] transferred into our stock of HeLa by cocultivation with MaTu cells treated with mitomycin C, to ensure that control and MaTu-infected cells were comparable. MaTu cells were incubated for 3 hours at 37°C in media with 5 μg/ml of mitomycin C [Calbiochem; LaJolla, CA (USA)]. Mixed cultures were set to 2×10^5 of mitomycin C-treated cells and 4×10^5 of fresh recipient cells in 5 ml of medium. After 3 days they were first subcultured and further passaged 1-2 times weekly.

Control HeLa cells were the same as those described in Zavada et al. (1972), supra.

Sera

Human sera from cancer patients, from patients suffering with various non-tumor complaints and from healthy women were obtained from the Clinics of Obstetrics and Gynaecology at the Postgraduate Medical School, Bratislava, Czechoslovakia. Human sera KH was from a fifty year old

mammary carcinoma patient, fourteen months after resection. That serum was one of two sera out of 401 serum samples that contained neutralizing antibodies to the VSV(MaTU) pseudotype as described in Zavada et al. (1972), supra. Serum L8 was from a patient with Paget's disease. Serum M7 was from a healthy donor.

Rabbit anti-MaTu serum was prepared by immunizing a rabbit three times at intervals of 30 days with 10-5 x 10^7 viable MaTu-infected HeLa cells.

RIP and PAGE

RIP and PAGE were performed essentially as described in Zavada and Zavadova, supra, except that in the experiments described herein [^{35}S]methionine (NEN), 10 μCi/ml of methionine-free MEM medium, supplemented with 2% FCS and 3% complete MEM were used. Confluent petri dish cultures of cells were incubated overnight in that media.

For RIP, the SAC procedure [Kessler, J. Immunol., 115: 1617-1624 (1975)] was used. All incubations and centrifugations were performed at 0-4°C. Cell monolayers were extracted with RIPA buffer (0.14 M NaCl, 7.5 mM phosphate buffer, pH 7.2, 1% Triton X-100, 0.1% sodium deoxycholate, 1 mM phenylmethylsulfonyl fluoride and Trasylol). To reduce non-specific reactions, antisera were preabsorbed with fetal calf serum [Barbacid et al., PNAS

(USA), 77: 1617-1621 (1980)] and antigenic extracts with SAC.

For PAGE (under reducing conditions) we used 10% gels with SDS [Laemmli, Nature, 227: 680-685 (1970)]. As reference marker proteins served the Sigma kit [product MW-SDS-200; St. Louis, MO (USA)]. For fluorography we used salicylate [Heegaard et al., Electrophoresis, 5: 263-269 (1984)].

Immunoblots

Immunoblotting used as described herein follows the method of Towbin et al., PNAS (USA), 76: 4350-4354 (1979). The proteins were transferred from the gels onto nitrocellulose [Schleicher and Schuell; Dassel Germany; 0.45 μm porosity] in Laemmli electrode buffer diluted 1:10 with distilled water, with no methanol or SDS. The transfer was for 2 1/2 hours at 1.75 mA/cm^2. The blots were developed with ^{125}I-labeled MAbs and autoradiography was performed using intensifying screens, with X-ray films exposed at -70°C.

In extracts from cell cultures containing only small amounts of MN antigen, we concentrated the antigen from 0.5 or 1 ml of an extract by adding 50 μl of a 10% SAC suspension, pre-loaded with MAb M75. This method allowed the concentration of MN antigen even from clinical specimens, containing human IgG; preliminary control

experiments showed that such a method did not interfere with the binding of the MN antigen to SAC-adsorbed M75. Tissue extracts were made by grinding the tissue with a mortar and pestle and sand (analytical grade). To the homogenates was added RIPA buffer, 10:1 (volume to weight) of original tissue. The extracts were clarified for 3 minutes on an Eppendorf centrifuge.

Example 1

Immunofluorescence of MaTu-Specific Antigens

Immunofluorescence experiments were performed on control and MaTu-infected HeLa cells with monoclonal antibodies, prepared as described above, which are specific for MaTu-related antigens. FITC-conjugated anti-mouse IgG was used to detect the presence of the monoclonal antibodies. Staining of the cells with Giemsa revealed no clear differences between control and MaTu-infected HeLa cells.

MAbs, which in preliminary tests proved to be specific for MaTu-related antigens, showed two different reactivities in immunofluorescence. A representative of the first group, MAb M67, gave a granular cytoplasmic fluorescence in MaTu-infected HeLa, which was only seen in cells fixed with acetone; living cells showed no fluorescence. MAb M16 gave the same type of fluorescence.

With either M67 or M16, only extremely weak "background" fluorescence was seen in control HeLa cells.

Another MAb, M75, showed a granular membrane fluorescence on living MaTu-infected cells and a granular nuclear fluorescence in acetone-fixed cells. However, M75 sometimes showed a similar, although much weaker, fluorescence on uninfected HeLa cells. A relationship was observed based upon the conditions of growth: in HeLa cells uninfected with MaTu, both types of fluorescence with MAb M75 were observed only if the cells were grown for several passages in dense cultures, but not in sparse ones.

The amount of M75-reactive cell surface antigen was analyzed cytofluorometrically and was dependent on the density of the cell cultures and on infection with MaTu. Control and MaTu infected HeLa cells were grown for 12 days in dense or sparse cultures. The cells were released with Versene (EDTA), and incubated with MAb M75 or with no MAb, and subsequently incubated with FITC-conjugated anti-mouse IgG. The intensity of fluorescence was measured.

It appeared that the antigen binding MAb M75 is inducible: it was found to be absent in control HeLa grown in sparse culture, and to be induced either by the growth of HeLa in dense culture or by infection with MaTu. Those two factors were found to have an additive or synergistic effect. Those observations indicated along with other results described herein that there were two different

agents involved: exogenous, transmissible MX, reactive with M67, and endogenous, inducible MN, detected by MAb M75.

Example 2

Immunoblot Analysis of Protein(s) Reactive with MAb M75

To determine whether MAb M75 reacts with the same protein in both uninfected and MaTu-infected HeLa, and to determine the molecular weight of the protein, extracts of those cells were analyzed by PAGE and immunoblotting (as described above). HeLa cells uninfected or MaTu-infected, that had been grown for 12 days in dense or sparse cultures, were seeded in 5-cm petri dishes, all variants at 5 x 10^5 cells per dish. Two days later, the cells were extracted with RIPA buffer (above described), 200 μl/dish. The extracts were mixed with 2x concentrated Laemmli sample buffer containing 6% mercaptoethanol and boiled for five minutes. Proteins were separated by SDS-PAGE and blotted on nitrocellulose. The blots were developed with ^{125}I-labeled MAb M75 and autoradiography.

MAb M75 reacted with two MN-specific protein bands of 54 kd and 58 kd, which were the same in uninfected HeLa grown at high density and in MaTu-infected HeLa, evidencing that M75 recognizes the same protein(s) in both uninfected and MaTu-infected HeLa cells. Consistent with the cytofluorometric results, the amount of the antigen depended

both on cell density and on infection with MaTu, the latter being a much more potent inducer of p54/58N.

Example 3

Radioimmunoassay of MaTu-Specific Antigens In Situ

In contrast to the results with M75, the other MAb, M67, appeared to be specific for the exogenous, transmissible agent MX. With M67 we observed no immunofluorescence in control HeLa, regardless of whether the cells were grown in dense or in sparse culture. That difference was clearly evidenced in radioimmunoassay experiments wherein ^{125}I-labeled MAbs M67 and M75 were used.

For such experiments, parallel cultures of uninfected and MaTu-infected cells were grown in dense or sparse cultures. The cultures were either live (without fixation), or fixed (with methanol for five minutes and air-dried). The cultures were incubated for two hours in petri dishes with the ^{125}I-labeled MAbs, 6 x 10^4 cpm/dish. Afterward, the cultures were rinsed four times with PBS and solubilized with 1 ml/dish of 2 N NaOH, and the radioactivity was determined on a gamma counter.

The simple radioimmunoassay procedure of this example was performed directly in petri dish cultures. Sixteen variants of the radioimmunoassay enabled us to determine whether the MX and MN antigens are located on the surface or in the interior of the cells and how the

expression of those two antigens depends on infection with MaTu and on the density, in which the cells had been grown before the petri dishes were seeded. In live, unfixed cells only cell surface antigens can bind the MAbs. In those cells, M67 showed no reaction with any variant of the cultures, whereas M75 reacted in accord with the results of Examples 1 and 2 above.

Fixation of the cells with methanol made the cell membrane permeable to the MAbs: M67 reacted with HeLa infected with MaTu, independently of previous cell density, and it did not bind to control HeLa. MAb M75 in methanol-fixed cells confirmed the absence of corresponding antigen in uninfected HeLa from sparse cultures and its induction both by growth in dense cultures and by infection with MaTu.

Example 4

Identification of MaTu Components Reactive with Animal Sera or Associated with VSV Virions

Immunoblot analyses of MaTu-specific proteins from RIPA extracts from uninfected or MaTu-infected HeLa and from purified VSV reproduced in control or in MaTu-infected HeLa, identified which of the antigens, p58X or p54/58N, were radioimmunoprecipitated with animal sera, and which of them was responsible for complementation of VSV mutants and for the formation of pseudotype virions. Details concerning the

procedures can be found in Pastorekova et al., Virology, 187: 620-626 (1992).

The serum of a rabbit immunized with MaTu-infected HeLa immunoprecipitated both MAb M67- and MAb M75-reactive proteins (both p58X and p54/58N), whereas the "spontaneously" immune sera of normal rabbit, sheep or leukemic cow immunoprecipitated only the M67-reactive protein (p58X). On the other hand, in VSV reproduced in MaTu-infected HeLa cells and subsequently purified, only the M75-reactive bands of p54/58N were present. Thus, it was concluded that MX and MN are independent components of MaTu, and that it was p54/58N that complemented VSV mutants and was assembled into pseudotype virions.

As shown in Figure 6 discussed below in Example 5, MX antigen was found to be present in MaTu-infected fibroblasts. In Zavada and Zavadova, supra, it was reported that a p58 band from MX-infected fibroblasts could not be detected by RIP with rabbit anti-MaTu serum. That serum contains more antibodies to MX than to MN antigen. The discrepancy can be explained by the extremely slow spread of MX in infected cultures. The results reported in Zavada and Zavadova, supra were from fibroblasts tested 6 weeks after infection, whereas the later testing was 4 months after infection. We have found by immunoblots that MX can be first detected in both H/F-N and H/F-T hybrids after 4

weeks, in HeLa cells after six weeks and in fibroblasts only 10 weeks after infection.

Example 5

Expression of MN- and MX- Specific Proteins

Figure 6 graphically illustrates the expression of MN- and MX- specific proteins in human fibroblasts, in HeLa cells and in H/F-N and H/F-T hybrid cells, and contrasts the expression in MX-infected and uninfected cells. Cells were infected with MX by co-cultivation with mitomycin C-treated MX-infected HeLa. The infected and uninfected cells were grown for three passages in dense cultures. About four months after infection, the infected cells concurrently with uninfected cells were grown in petri dishes to produce dense monolayers.

A radimmunoassay was performed directly in confluent petri dish (5 cm) culture of cells, fixed with methanol essentially as described in Example 3, supra. The monolayers were fixed with methanol and treated with ^{125}I-labeled MAbs M67 (specific for exogenous MX antigen) or M75 (specific for endogenous MN antigen) at 6 x 10^4 cpm/dish. The bound radioactivity was measured; the results are shown in Figure 6.

Figure 6 shows that MX was transmitted to all four cell lines tested, that is, to human embryo fibroblasts, to HeLa and to both H/F-N and H/F-T hybrids; at the same time,

all four uninfected counterpart cell lines were MX-negative (top graph of Figure 6). MN antigens are shown to be present in both MX-infected and uninfected HeLa and H/F-T cells, but not in the fibroblasts (bottom graph of Figure 6). No MN antigen was found in the control H/F-N, and only a minimum increase over background of MN antigen was found in MaTu infected H/F-N. Thus, it was found that in the hybrids, expression of MN antigen very strongly correlates with tumorigenicity.

Those results were consistent with the results obtained by immunoblotting as shown in Figure 7. The MN-specific twin protein p54/58N was detected in HeLa cell lines (both our standard type, that is, HeLa K, and in the Stanbridge mutant HeLa, that is, D98/AH.2 shown as HeLa S) and in tumorigenic H/F-T; however, p54/58N was not detected in the fibroblasts nor in the non-tumorigenic H/F-N even upon deliberately long exposure of the film used to detect radioactivity. Infection of the HeLa cells with MX resulted in a strong increase in the concentration of the p54/58N protein(s).

The hybrid cells H/F-N and H/F-T were constructed by Eric J. Stanbridge [Stanbridge et al., Somatic Cell Genetics, 7: 699-712 (1981); and Stanbridge et al., Science, 215: 252-259 (1982)]. His original hybrid, produced by the fusion of a HeLa cell and a human fibroblast was not tumorigenic in nude mice, although it retained some

properties of transformed cells, for example, its growth on soft agar. Rare segregants from the hybrid which have lost chromosome 11 are tumorigenic. The most likely explanation for the tumorigenicity of those segregants is that chromosome 11 contains a suppressor gene (an antioncogene), which blocks the expression of a as yet unknown oncogene. The oncoprotein encoded by that oncogene is critical for the capacity of the H/F hybrids to produce tumors in nude mice. Since the p54/58N protein shows a correlation with the tumorigenicity of H/F hybrids, it is a candidate for that putative oncoprotein.

Example 6

Immunoblots of MN Antigen from Human Tumor Cell Cultures and from Clinical Specimens of Human Tissues

The association of MN antigen with tumorigenicity in the H/F hybrid cells as illustrated by Example 5 prompted testing for the presence of MN antigen in other human tumor cell cultures and in clinical specimens. Preliminary experiments indicated that the concentration of MN antigen in the extracts from other human tumor cell cultures was lower than in HeLa; thus, it was realized that long exposure of the autoradiographs would be required. Therefore, the sensitivity of the method was increased by the method indicated under Materials and Methods: Immunoblotting,

supra, wherein the MN antigen was concentrated by precipitation with MAb M75-loaded SAC.

Figure 8 shows the immunoblots wherein lane A, a cell culture extract from MX-infected HeLa cells was analysed directly (10 µl per lane) whereas the antigens from the other extracts (lanes B-E) were each concentrated from a 500 µl extract by precipitation with MAb M75 and SAC.

Figure 8 indicates that two other human carcinoma cell lines contain MN-related proteins -- T24 (bladder carcinoma; lane C) and T47D (mammary carcinoma; lane D). Those cells contain proteins which react with MAb M75 that under reducing conditions have molecular weights of 54 kd and 56 kd, and under non-reducing conditions have a molecular weight of about 153 kd. The intensity of those bands is at least ten times lower than that for the p54/58N twin protein from HeLa cells.

An extremely weak band at approximately 52 kd could be seen under reducing conditions from extracts from human melanoma cells (SK-Mel 1477;lane E), but no bands for human fibroblast extracts (lane B) could be seen either on the reducing or non-reducing gels.

Figure 9 shows immunoblots of human tissue extracts including surgical specimens as compared to a cell extract from MX-infected HeLa (lane A). The MN-related antigen from all the extracts but for lane A (analysed directly at 10 µl per lane) was first concentrated from a 1